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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:00:55 ; Search time 38 Seconds

(Without alignments)
1202.762 Million cell updates/sec

Title: US-10-086-156-24

Perfect score: 1780
Sequence: 1 NTMAVLRNRKGGKGPLRRRP.....NNEKSPVQLPAGVFQHPMG 343

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: A.Geneset.101002.*
2: /SID2/gcgdata/geneeq/geneeqp-emb1/AA1980.DAT.*
3: /SID2/gcgdata/geneeq/geneeqp-emb1/AA1981.DAT.*
4: /SID2/gcgdata/geneeq/geneeqp-emb1/AA1983.DAT.*
5: /SID2/gcgdata/geneeq/geneeqp-emb1/AA1984.DAT.*
6: /SID2/gcgdata/geneeq/geneeqp-emb1/AA1985.DAT.*
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8: /SID2/gcgdata/geneeq/geneeqp-emb1/AA1987.DAT.*
9: /SID2/gcgdata/geneeq/geneeqp-emb1/AA1988.DAT.*
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16: /SID2/gcgdata/geneeq/geneeqp-emb1/AA1995.DAT.*
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18: /SID2/gcgdata/geneeq/geneeqp-emb1/AA1997.DAT.*
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20: /SID2/gcgdata/geneeq/geneeqp-emb1/AA1999.DAT.*
21: /SID2/gcgdata/geneeq/geneeqp-emb1/AA2000.DAT.*
22: /SID2/gcgdata/geneeq/geneeqp-emb1/AA2001.DAT.*
23: /SID2/gcgdata/geneeq/geneeqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	915.5	51.4	271	21	AA15537 Human immune system
2	305	17.1	56	22	ABB28752 Peptide #1403 enco
3	305	17.1	56	22	ABB33939 Peptide #1445 enco
4	305	17.1	56	22	ABB19375 Protein #1374 enco
5	305	17.1	56	22	AA154702 Human brain expts
6	305	17.1	56	22	AA167102 Human bone marrow
7	305	17.1	56	22	AA14963 Peptide #1397 enco
8	305	17.1	56	22	AA127397 Peptide #1434 enco
9	305	17.1	56	22	AA102689 Peptide #1371 enco
10	305	17.1	56	23	ABG36762 Human peptide enco

11	282	15.8	190	22	ABG16368 Novel human diagno
12	278	15.6	197	22	AA673901 Human colon cancer
13	278	15.6	255	22	AAE04891 Human transporter
14	278	15.6	255	23	ABP51810 Human potassium ch
15	278	15.6	258	21	AB41622 Human ORF1386
16	245	13.8	175	21	AA153339 Human colon cancer
17	244.5	13.7	130	22	AA125242 Human protein sequ
18	215	12.1	76	21	AA103290 Human secreted pro
19	214	12.0	146	22	AA11265 Human Edp1 protein
20	211.5	11.9	237	20	AA134129 Human potassium ch
21	211.5	11.9	237	22	AA127754 Human full-length
22	211.5	11.9	237	22	AA193682 Human polypeptide
23	211.5	11.9	237	22	AA195201 Human polypeptide
24	211.5	11.9	237	22	AA195311 Human polypeptide
25	211.5	11.9	252	23	AA195311 Human polypeptide
26	206.5	11.6	237	22	AA193832 Human polypeptide
27	206	11.6	310	22	AA194003 Human stomach canc
28	206	11.6	310	22	AA194285 Human protein sequ
29	204	11.5	323	23	AA194285 Human protein sequ
30	204	11.5	329	22	AA193908 Human NSI protein s
31	199.5	11.2	272	22	AA125877 Human polypeptide
32	198.5	11.2	339	22	AA110329 Human transporter
33	196	11.0	301	22	AB10329 Human protein sequ
34	190	10.7	150	23	AB10329 Human protein sequ
35	189.5	10.6	338	22	AB10329 Human protein sequ
36	188.5	10.6	289	20	AA195954 Human endometrium
37	180.5	10.1	228	22	AB10329 Human protein sequ
38	180	10.1	289	21	AA13411 Arabidopsis thalia
39	180	10.1	298	21	AA13411 Arabidopsis thalia
40	180	10.1	324	21	AA13409 Arabidopsis thalia
41	180	10.1	396	21	AA13409 Arabidopsis thalia
42	180	10.1	402	21	AA13409 Arabidopsis thalia
43	180	10.1	504	21	AA13409 Arabidopsis thalia
44	180	10.1	707	22	AA13409 Arabidopsis thalia
45	176	9.9	305	22	AA193493 Human polypeptide,

ALIGNMENTS

RESULT 1
ID AAB15537 standard; Protein; 271 AA.
XX AAB15537;
AC AAB15537;
XX AAB15537;
DT 28-FEB-2001 (first entry)
XX AAB15537;
DE Human immune system molecule from incyte clone 2751129.
XX AAB15537;
KW Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianemic;
KW antiarteriosclerotic; antiaesthetic; antidiabetic; nephrotoxic; cancer;
KW antitumor; dermatological; antichryoid; virucide; hepatotropic; antibacterial;
KW gene therapy; diagnostic; immunological disorder; viral infection;
KW bacterial infection; fungal infection; parasitic infection; immunogen.
XX Homo sapiens.
XX WO2000060080-A2.
XX 12-OCT-2000.
XX 04-APR-2000; 2000WO-US09072.
XX 05-APR-1999; 99US-0127852.
XX 05-MAY-1999; 99US-0132647.
XX (INCY-) INCYTE PHARM INC.
XX Yue H, Lal P, Tang YT, Baughn KR, Azimzal Y, Lu DM;
XX WPI, 2000-665005/64.

DR N-PSDB; AAA95776.

XX New human immune system molecules 1-15 and polynucleotides encoding
 PT them useful for diagnosing, treating or preventing e.g. immunological
 PT disorders, infections, cell proliferative disorders, microbial
 PT infections

XX Claim 1; Page 77; 95pp; English.

XX This sequence represents a human immune system molecule (IMOL) encoded
 CC by the CDNA isolated as clone 2751129 from the Incyte THPLAZS08 library.
 CC The human IMOLs (AA815536-815550) and their encoding polynucleotides
 CC (AA95775-895789), and compositions comprising them are useful for the
 CC diagnosis, treatment or prevention of immunological disorders,
 CC infections and cell proliferative disorders, including cancer. The IMOL
 CC may be used to treat or prevent disorders associated with decreased
 CC expression or activity of IMOL, such as immunological disorders
 CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),
 CC hematopoietic cancer, infections caused by virus (e.g. adenovirus,
 CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,
 CC Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g.
 CC Plasmodium, Trypanosoma, intestinal protozoa), cell proliferative
 CC disorders (e.g. actinic keratosis, arteriosclerosis, hirsutis), and
 CC cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also
 CC useful as immunogens for the development of antibodies that
 CC specifically recognize these peptides. The polynucleotides may be used
 CC to detect and quantify gene expression in biopsied tissues in which
 CC expression of IMOL may be correlated with the disease, as targets in a
 CC microarray, to detect differences in gene sequences among normal,
 CC carrier and affected individuals, and for screening libraries of
 CC compounds in drug screening techniques. Antibodies which specifically
 CC bind to IMOL may be used for the diagnosis of disorders characterized
 CC by expression of IMOL, or in assays to monitor patients being treated
 CC with IMOL or agonists, antagonists, or inhibitors of IMOL.

XX Sequence 271 AA:

SO Query Match 51.4%; Score 915.5; DB 21; Length 271;
 Best Local Similarity 88.0%; Pred. No. 3,3e-74;
 Matches 184; Conservative 3; Mismatches 17; Indels 5; Gaps 2;

QY 96 MYYVYGRSDSRQDGMSSSDAEDFLPEATPTAQAGHALPLPQEPFVYVPLNTGGA 155
 DB 1 MYYVYGRSDSRQDGMSSSDAEDFLPEATPTAQAGHALPLPQEPFVYVPLNTGGA 60
 QY 156 HTTTLSTLCRCYEDTMLAMFSGRHYIPTDSEGRYFTDRDGTGHDVNLFRSGDLPPRE 215
 DB 61 HTTTLSTLCRCYEDTMLAMFSGRHYIPTDSEGRYFTDRDGTGHDVNLFRSGDLPPRE 120
 QY 216 RYRAVYKEAQYVTAIGPLLEQLENMOPKGRVQAQFGLMPYKDHLEIVEIAR-LRAV 274
 DB 121 RYRAVYKEAQYVTAIGPLLEQLENMOPKGRVQAQFGLMPYKDHLEIVEIARCVRSS 180
 QY 275 QRKA----RFAKIKSLTPSWLMSVLKMP 299
 DB 181 GRPALPSSRSVSSRRCPSPPMVSRSSTP 209

RESULT 2
 ID ABB28752 standard; Peptide; 56 AA.
 AC ABB28752;
 DT 01-FEB-2002 (first entry)
 DE Peptide #1403 encoded by breast cell single exon nucleic acid probe.
 XX Human; microarray; single exon probe; gene expression; breast;
 KW disease; cancer.
 OS Homo sapiens.
 XX

PN W0200157271-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00662.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes,
 PT useful for measuring gene expression in sample derived from human
 PT breast, comprises number of single exon nucleic acid probes

XX Claim 27; SEQ ID NO 11720; 327bp + sequence listing; English.

XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting
 CC the probes with a collection of detectably labelled nucleic acids
 CC derived from mRNA of human breast, and then measuring the label
 CC bound to each probe of the microarray. The probes are useful for
 CC verifying the expression of regions of genomic DNA predicted to
 CC encode proteins. They are useful for gene discovery, and for
 CC determining predisposition and/or prognosis breast disease. Gene
 CC expression analysis is useful for assessing the toxicity of chemical
 CC agents on cells. The microarray of this invention presents a far greater
 CC diversity of probes for measuring gene expression, with far less bias
 CC than expressed sequence tag microarrays. The method is suitable for
 CC rapid production of functional information from genomic sequence. The
 CC present sequence is a peptide encoded by a single exon nucleic acid
 CC probe of the invention.

CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 56 AA;

SO Query Match 17.1%; Score 305; DB 22; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3,7e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 FPEVYVPLNTGGAHFTTTLSTLCRCYEDTMLAMFSGRHYIPTDSEGRYFTDRDGTGTF 199
 DB 1 FPEVYVPLNTGGAHFTTTLSTLCRCYEDTMLAMFSGRHYIPTDSEGRYFTDRDGTGTF 56

RESULT 3
 ID ABB33939 standard; Peptide; 56 AA.
 AC ABB33939;
 DT 04-FEB-2002 (first entry)
 DE Peptide #1445 encoded by human foetal liver single exon probe.
 XX Human; foetal liver; gene expression; single exon nucleic acid probe.
 KW Homo sapiens.
 OS W0200157271-A2.
 XX

PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 26574; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX fetal liver. The present sequence is a peptide encoded by a single exon
XX nucleic acid probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 56 AA;

Query Match 17.1%; Score 305; DB 22; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.7e-20;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 FPEVPLNIGAHFTTRLTSLRCYEDTMAAFSGRHYIPTDSEGRYFIDRDGTHF 199
DB 1 FPEVPLNIGAHFTTRLTSLRCYEDTMAAFSGRHYIPTDSEGRYFIDRDGTHF 56

RESULT 4

ABBI9375
ID ABBI9375 standard; Protein; 56 AA.

AC ABBI9375;

DT 23-JAN-2002 (first entry)

DE Protein #1374 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease.

OS Homo sapiens.

PN WO200157274-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00666.

XX
XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX
PS Claim 15; SEQ ID NO 21145; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart (see
XX ABA21535-ABA41305). The present sequence is a protein encoded by one such
XX probe. The probes may be used for predicting, measuring and displaying
XX gene expression in samples derived from the human heart via microarrays.
XX By measuring gene expression, the probes are useful for predicting,
XX diagnosing, grading, staging, monitoring and prognosing diseases of the
XX human heart and vascular system e.g. cardiovascular disease,
XX hypertension, cardiac arrhythmias and congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 56 AA;

Query Match 17.1%; Score 305; DB 22; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.7e-20;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 FPEVPLNIGAHFTTRLTSLRCYEDTMAAFSGRHYIPTDSEGRYFIDRDGTHF 199
DB 1 FPEVPLNIGAHFTTRLTSLRCYEDTMAAFSGRHYIPTDSEGRYFIDRDGTHF 56

RESULT 5
AAMS4702
ID AAMS4702 standard; Protein; 56 AA.

AC AAMS4702;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26807.

XX Human; brain expressed exon; gene expression analysis; probe;

KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsy; cancer.

OS Homo sapiens.

PN WO200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00667.

XX
XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX
XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human

PT brains -
 XX
 PS Example 4; SEQ ID NO: 26807; 650bp + Sequence Listing; English.
 XX

CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention.

XX
 SQ Sequence 56 AA;

Query Match 17.1%; Score 305; DB 22; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3,7e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 144 FPEVPLNIGAGHFTTSLRCYEDTMLAMFGSRHYIPTDSGRYFIDRDGTHF 199
 DB 1 FPEVPLNIGAGHFTTSLRCYEDTMLAMFGSRHYIPTDSGRYFIDRDGTHF 56

RESULT 6
 AAM67102
 ID AAM67102; standard; Protein; 56 AA.

XX
 AC AAM67102;

DT 06-NOV-2001 (first entry)

XX Human bone marrow expressed probe encoded protein SEQ ID NO: 27408.

KM Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukemia; lymphoma; myeloma.

XX Homo sapiens.

XX WO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00666.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human bone marrow -

XX Example 4; SEQ ID NO: 27408; 658bp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.

XX
 SQ Sequence 56 AA;

Query Match 17.1%; Score 305; DB 22; Length 56;

Best Local Similarity 100.0%; Pred. No. 3,7e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 144 FPEVPLNIGAGHFTTSLRCYEDTMLAMFGSRHYIPTDSGRYFIDRDGTHF 199
 DB 1 FPEVPLNIGAGHFTTSLRCYEDTMLAMFGSRHYIPTDSGRYFIDRDGTHF 56

RESULT 7

AM14963
 ID AM14963 standard; Protein; 56 AA.

XX
 AC AM14963;

DT 12-OCT-2001 (first entry)

XX Peptide #1397 encoded by probe for measuring cervical gene expression.

XX Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.

XX Homo sapiens.

XX WO200157278-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00670.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human cervical epithelial cells -

XX Claim 27; SEQ ID NO 19789; 487bp; English.

XX The present invention relates to human single exon nucleic acid probes
 CC (SENPs: see AAI10068-AA128459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 56 AA;

Query Match 17.1%; Score 305; DB 22; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3,7e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 144 FPEVPLNIGAGHFTTSLRCYEDTMLAMFGSRHYIPTDSGRYFIDRDGTHF 199
 DB 1 FPEVPLNIGAGHFTTSLRCYEDTMLAMFGSRHYIPTDSGRYFIDRDGTHF 56

RESULT 8
 AAM27397

ID AAM27397 standard; Protein; 56 AA.
 AC AAM27397;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Peptide #1434 encoded by probe for measuring placental gene expression.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 KM genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200157272-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00663.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488897/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human placenta.
 PS
 SQ Claim 27; SEQ ID No 27666; 654bp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENP;
 CC see A113135-A1157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.
 CC
 SQ Sequence 56 AA;
 XX
 XX
 Query Match 17.1%; Score 305; DB 22; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3.7e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 144 FPEVPLNIGAHFTTRLSTLCYEDTMAAMFSGRHYIPTDSEGRYFIDRDGTHF 199
 DB 1 FPEVPLNIGAHFTTRLSTLCYEDTMAAMFSGRHYIPTDSEGRYFIDRDGTHF 56
 XX
 XX
 RESULT 9
 ID AAM02689 standard; Protein; 56 AA.
 AC AAM02689;
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE Peptide #1371 encoded by probe for measuring breast gene expression.
 XX
 KW Probe; human; breast disease; breast cancer; development disorder;
 KM inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200157270-A2.
 XX

PD 09-AUG-2001.
 XX
 XX 29-JAN-2001; 2001WO-US00661.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-476286/51.
 XX
 PT Novel single exon nucleic acid probe used to measuring gene expression
 XX in a human breast.
 PS
 SQ Claim 27; SEQ ID No 11429; 322bp; English.
 XX
 CC The present invention relates to novel single exon nucleic acid probes
 CC (see A1100010-A110067). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for measuring human gene expression in a
 CC human breast sample, where the probe hybridises at high stringency to a
 CC nucleic acid expressed in the human breast. The probes are useful for
 CC predicting, diagnosing, grading, staging, monitoring and prognosis
 CC diseases of the human breast, particularly those diseases with polygenic
 CC aetiology. The diseases include: breast cancer; disorders of development,
 CC inflammatory diseases of the breast, fibrocystic changes, proliferative
 CC breast disease and non-carcinoma tumours.
 CC
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 56 AA;
 XX
 XX
 Query Match 17.1%; Score 305; DB 22; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3.7e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 144 FPEVPLNIGAHFTTRLSTLCYEDTMAAMFSGRHYIPTDSEGRYFIDRDGTHF 199
 DB 1 FPEVPLNIGAHFTTRLSTLCYEDTMAAMFSGRHYIPTDSEGRYFIDRDGTHF 56
 XX
 XX
 RESULT 10
 ID ABG36762 standard; Peptide; 56 AA.
 AC ABG36762;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 26427.
 XX
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberculous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsagen syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200186003-A2.
 XX
 PD 15-NOV-2001.

XX 30-JAN-2001; 2001WO-0500665.
XX
XX 04-FEB-2000; 2000US-180312P.
XX 26-MAY-2000; 2000US-207456F.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-234687P.
XX 27-SEP-2000; 2000US-236359P.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples -
XX
XX Claim 27; SEQ ID NO 26427; 634bp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of
XX probes; the novel set of probes which hybridize at high stringency to a
XX nucleic acid expressed in the human lung; measuring gene expression in a
XX sample derived from human lung, comprising (a) contacting the array with
XX a collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of
XX the array; identifying exons in a eukaryotic genome, comprising
XX (a) algorithmically predicting at least one exon from genomic sequences
XX of the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORF). The probes are used for gene
XX expression analysis, and for identifying exons in a gene, particularly
XX using human lung derived mRNA and for the study of lung diseases
XX such as asthma, lung cancer, chronic obstructive pulmonary disease
XX (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
XX fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
XX Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
XX haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
XX pulmonary alveolar proteinosis, Kartagener syndrome, fibrocystic
XX pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
XX and hyaline membrane disease. The present sequence is a peptide/protein
XX encoded by a single exon probe of the invention.
XX Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic
XX format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 56 AA;
XX
XX Query Match 17.1%; Score 305; DB 23; Length 56;
XX Best Local Similarity 100.0%; Pred. No. 3.7e-20;
XX Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 144 FEVYVPLNIGGAHFTTRLTSTLCYEDTMTAAFGSGRHRYPTDSGRTFIDRGTHF 199
XX ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
XX DB 1 FEVYVPLNIGGAHFTTRLTSTLCYEDTMTAAFGSGRHRYPTDSGRTFIDRGTHF 56

RESULT 11
ABG16368
ID ABG16368 standard; Protein; 190 AA.
XX
XX ABG16368;
XX
XX 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #16359.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX N-PSDB; AAS80555.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 20; SEQ ID NO 46727; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers, and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 190 AA;
XX
XX Query Match 15.8%; Score 282; DB 22; Length 190;
XX Best Local Similarity 37.6%; Pred. No. 2.7e-11;
XX Matches 71; Conservative 34; Mismatches 66; Indels 18; Gaps 4;
XX
XX 87 PGARRRAGNVVYVGREDSRQDAMSSDAEDDFEPATPTAQACHALPLQGEPE 146
XX ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
XX DB 5 PGALPLAVITAMGCAVE--RPVGSMTSQTFPLQSPRPAPRTMS-----T 48
XX ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
XX 147 VPLNIGGAHFTTRLTSTLCYEDTMTAAFGSGRHRYPTDSGRTFIDRGTHFGDVNL 206

Db 49 VEEINVGEEHTTTLGTRKFPKSLAEMSSSLAKASTDAEGRFFIDRPPSTYFRPILDYL 108
 QY 207 RSGCLPRERRVAYKRAQYAIAPLLEOLENMPKGERY-ROAFLGLMPYKDLERI 265
 Db 109 RTQGV-PTQHPPEYRRAQFEIKRIVKLEDMQIFGEVSRQFLQVGYSENLELM 167
 QY 266 VEIARLRAV 274
 Db 168 VRLARAEAI 176

RESULT 12
 AAG73901
 ID AAG73901 standard; Protein; 197 AA.
 XX AAG73901;
 AC AAG73901;
 DF 03-SEP-2001 (first entry)
 DE Human colon cancer antigen protein SEQ ID NO:4665.
 XX Human colon cancer antigen protein SEQ ID NO:4665.
 KM Human colon cancer; colon cancer antigen; diagnosis; detection;
 KM colorectal carcinoma.
 XX Homo sapiens.
 OS Homo sapiens.
 PN MO200122920-A2.
 XX 05-APR-2001.
 PD 28-SEP-2000; 2000OWO-US26524.
 PF 29-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-0163280.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Ruben SM, Barash SC, Birse CE, Rosen CA;
 PI N-PSDB; AAH33332.
 DR N-PSDB; AAH33332.
 XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -
 PS Claim 11; Page 6463-6464; 9803pp; English.

CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patient's own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated Ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAH77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.

XX Sequence 197 AA;
 SQ Query Match 15.6%; Score 278; DB 22; Length 197;
 Best Local Similarity 39.3%; Pred. No. 6,5e-17;
 Matches 66; Conservative 29; Mismatches 57; Indels 16; Gaps 3;

QY 108 RODGAMSSSDADDLEPPTATQAGHALPLLPQEPPEVVPINIGAHETTRILSTLCRY 167
 Db 12 REVGMTSQTPIPOSEPRPPTMS-----TWELNVGGEHTTTLGTRKF 57
 QY 168 EDTMLAAMFSGNHVPTDESGRYFTDQGHGVDLNFRLSGDLPRERRVAYKRAQY 227
 Db 58 PGSKLEMFSSSLAKASTDAEGRFFIDRPPSTYFRPILDYLTQGV-PTQHPPEYRRAQFY 116
 QY 228 AIGPLLEOLENMPKGERY-ROAFLGLMPYKDLERIYIARLRAV 274
 Db 117 EIKPLVKLEDMQIFGEVSRQFLQVGYSENLELMVRLARAEAI 164

RESULT 13
 AAE04891
 ID AAE04891 standard; Protein; 255 AA.
 XX AAE04891;
 AC AAE04891;
 DF 10-SEP-2001 (first entry)
 DE Human transporter and ion channel-4 (TRICH-4) protein.
 XX Human transporter and ion channel-4 (TRICH-4) protein.
 KM Human; transporter and ion channel-4; TRICH-4; vaccine; cystic fibrosis;
 KM gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy;
 KM hypertension; angina; neurological disorder; asthma; bipolar disorder;
 KM dementia; depression; Alzheimer's disease; epilepsy; mood; arrhythmia;
 KM Pick's disease; ischemic cerebrovascular disease; AIDS; anxiety; stroke;
 KM Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy;
 KM demyelinating disease; mental disorder; schizophrenia; polymyositis;
 KM muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease;
 KM dermatomyositis; diabetes mellitus; immunological disorder; psoriasis;
 KM rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus;
 KM sickle cell anaemia; Wilson's disease; infertility; Cushing's disease;
 KM scleroderma; pulmonary artery stenosis; nocturnal; Addison's disease;
 KM malabsorption syndrome; hypercholesterolemia; cancer.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200146258-A2.
 XX WO200146258-A2.
 PD 28-JUN-2001.
 XX 22-DEC-2000; 2000OWO-US35095.
 PF 23-DEC-1999; 99US-0172000.
 PR 14-JAN-2000; 2000US-0176083.
 PR 21-JAN-2000; 2000US-0177332.
 PR 28-JAN-2000; 2000US-0178572.
 PR 02-FEB-2000; 2000US-0179758.
 PR 10-FEB-2000; 2000US-0181625.
 XX (INCY-) INCYTE GENOMICS INC.
 PA Baughn MR, Burford N, Au-Young J, Lu DAM, Yang J, Reddy R, Lal P,
 PI Hillman JL, Azimzal Y, Yue H, Nguyen DB, Yao MG, Gandhi AR,
 PI Tang YL, Khan FA;
 XX WPI: 2001-418042/44.
 DR N-PSDB; AAD09555.
 XX Novel human transporter and ion channel proteins useful for treating
 PT and preventing transport, neurological, muscle and immunological
 PT disorders -
 PS Claim 1; Page 116-117; 160pp; English.

CC The present sequence is transporter and ion channel-4 (TRICH-4) protein.
 CC TRICH is used as vaccine. TRICH is useful for treating a disease or
 CC condition associated with decreased expression of functional TRICH,
 CC such as transport disorder including amyotrophic lateral sclerosis,
 CC cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth
 CC disease, Duchenne muscular dystrophy, angina and hypertension.

DR WPI; 2002-583519/62.

neurodegenerative disorder: graft vs host disease: osteoarthritis: cancer; proliferative disorder; hyperplasia; gene therapy; aneurysm; kw

KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.

OS Homo sapiens.

PN WO200058473-A2.

XX 05-OCT-2000.

PD 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 05-APR-1999; 99US-0127728.

PR 30-MAR-2000; 2000US-0540763.

XX (CUBA-) CUBAGEN CORP.

PI Shinkets RA, Leach M;

XX MPI; 2000-602362/57.

DR N-PSDB; AAC75831.

XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -

PS Claim 11; Page 2011-2012; 5507pp; English.

CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antiproliferative; antiparkinsonian; nocitropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressive;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

SO Sequence 258 AA;

Query Match 15.6%; Score 278; DB 21; Length 258;

Best Local Similarity 39.3%; Pred. No. 9.6e-17;

Matches 66; Conservative 29; Mismatches 57; Indels 16; Gaps 3;

QY 108 RODAMSSSDAEDDFLEPATPTAQAHALPLDQEPPEVPLNIGAGAFTRRLSTLRXY 167

DB 12 RPYGRMTSQTPLPSPRRPTMS-----TWELNVGGEHTTLTGTRKF 57

QY 168 EDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHRGVLANFLRSGDLPFRERVAVKEAQY 227

DB 58 PGSKLAKEFSSIAKASTAEGRFIDRSTYFRPIDYLRKGQV-PTQHIEVYREAGFY 116

QY 228 AIGPLLEQLEMMQPKGEKV-RQAFGLMPYTKDLEKIVEIARAV 274

DB 117 EIKPLVKLEDMPOIFGBOVSKOFLQVPGYSENLEIMVRLARAFAI 164

Search completed: February 12, 2003, 11:07:32
 Job time : 39 secs


```

: APPLICANT: Miller, Andrew P.
: APPLICANT: Curran, Mark Edward
: APPLICANT: Hu, Ping
: APPLICANT: Rutter, Marc
: APPLICANT: Wang, Jian-Wang
: TITLE OF INVENTION: No. 6399761el Human Potassium Channels
: FILE REFERENCE: SEQ-15P
: CURRENT APPLICATION NUMBER: US/09/336,643A
: PRIOR FILING DATE: 1999-06-18
: PRIOR APPLICATION NUMBER: 60/076,667
: PRIOR FILING DATE: 1998-08-07
: PRIOR APPLICATION NUMBER: 60/116,448
: PRIOR FILING DATE: 1999-01-19
: PRIOR APPLICATION NUMBER: PCT/US99/03826
: PRIOR FILING DATE: 1999-02-22
: NUMBER OF SEQ ID NOS: 87
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 12
: LENGTH: 256
: TYPE: PRT
: ORGANISM: H. sapiens
: US-9-336-643A-12

```

Query Match	9.6%	Score 170.5	DB 4	Length 258
Best Local Similarity	38.9%	Pred. No. 5.3e-09		
Matches 37	Conservative 22	Mismatches 33	Indels 3	Gaps 1

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0Y 147 VPPNIGAGHETTTTSLRCEDEDMALAMSGRAYITPDSGAEFYIDROGCHFGDYNTFL 206
    :::::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 34 LMTLWAGSYLTITKQKLTLPDFFLESGYNGKLTCPFDAGHFIIDROGLTPHYVNTFL 93

0Y 207 RSGDLPFRERVR---AVYKEQYATAPLLEOLEN 238
    :::::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 94 RNGEILLPEGRRENOLLAQAEIFFQTLGGLAEVYS 128

```

```

RESULT 3
US-09-166-350-12
; Sequence 12, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; TITLE OF INVENTION: Uses Therefor
; FILE REFERENCE: L0461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 812
; TYPE: prt
; ORGANISM: Homo sapiens
; US-09-166-350-12

```

Query Match	9.3%	Score 165;	DB 4;	Length 812;
Best Local Similarity	33.9%	Pred No. 1.1e-07;		
Matches 43;	Conservative 20;	Mismatches 60;	Indels 4;	Gaps 3

QY 134 GH--ALPLLEQEEPEVVP L NIGCAHETTRRLSTLCYEDYRLAAMFGSRHYIPTDSEGYE 191

DB 4 GHGCEFPAAAGSGEIVQLNVTGTRFSTRQTLNIPDSEFSSLLSGRISTLNDETGAIF 63

Qy 192 IDRDGTHFGVDLNFRLSGDLPPR-ERVRVAVYKKEAQYYAIGPLLEOLEENMPKGEKVQA 256
||| | : |||| : || : : || : || : | :
Db 64 IDRDPAAFAPILNLFRLKELDRLGVSIVNLRHEAFYGTIPPLVRRLDLCBELERSSCGSV 1232

QY	251	-FLGIMP	256
		↑ : ↑	
Db	124	LFHGYP	130

RESULT 4
US-09-336-643A-14
; Sequence 14, Application US/09336643A

```

1  APPLICANT: MILLER, Andrew P.
2  APPLICANT: Curran, Mark Edward
3  APPLICANT: Hu, Ping
4  APPLICANT: Rutter, Marc
5  APPLICANT: Wang, Jian-Wang
6  TITLE OF INVENTION: No. 63939761e1 Human Potassium Channels
7  FILE REFERENCE: SEQ-15P
8  CURRENT APPLICATION NUMBER: US/09/336,643A
9  CURRENT FILING DATE: 1999-06-18
10 PRIOR APPLICATION NUMBER: 60/076,687
11 PRIOR FILING DATE: 1998-08-07
12 PRIOR APPLICATION NUMBER: 60/116,448
13 PRIOR FILING DATE: 1999-01-19
14 PRIOR APPLICATION NUMBER: PCT/US99/03826
15 PRIOR FILING DATE: 1999-02-22
16 NUMBER OF SEQ ID NOS: 87
17 SOFTWARE: FASTSEQ for Windows Version 4.0
18 SEQ ID NO 14
19 LENGTH: 256
20 TYPE: PRT
21 ORGANISM: H. sapiens
22 FEATURE:
23 NAME/KEY: VARIANT
24 LOCATION: (1)...(256)
25 OTHER INFORMATION: Xaa = Any Amino Acid
26 US-09-336-643A-14

```

Query Match	8.8%	Score 157.5	DB 4	Length 256
Best Local Similarity	34.2%	Pred. No. 1e-07		
Matches 40	Conservative 25	Mismatches 47	Indels 5	Gaps 3

```

07 125 PATPATAGAHPLLPDPEPEVADPLNTGAMHTTBTSTLCEYDITMAAFSGRHVPT 186
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 10 PASPLANG-GIPIPAQLKSNAPHAIDVGMMHTSSLTATLKRYEBSRGRLDSTETVL 68

07 135 DS-BGRITIDRDGTHGCVTLNLSGDLPRBRYR--ATYKEAYTAIGLEOLE 237
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 69 DSLKHVYTHIDRGQFRIINLFRTSKLLIDDKRDYTLLEAKRYQLOPMLEME 125

```

RESULT 5
US-09-336-643A-27
; Sequence 27, Application US/09336643A
; Patent No. 6200761

```

1  APPLICANT: Miller, Andrew P.
2  APPLICANT: Curran, Mark Edward
3  APPLICANT: Hu, Ping
4  APPLICANT: Rutcer, Marc
5  APPLICANT: Wang, Jian-Wang
6  TITLE OF INVENTION: No. 6399761el Human Potassium Channel
7  FILE REFERENCE: SEQ-15P
8  CURRENT APPLICATION NUMBER: US/09/336,643A
9  CURRENT FILING DATE: 1999-06-18
10 PRIOR APPLICATION NUMBER: 60/076,687
11 PRIOR FILING DATE: 1998-08-07
12 PRIOR APPLICATION NUMBER: 60/116,448
13 PRIOR FILING DATE: 1999-01-19
14 PRIOR APPLICATION NUMBER: PCT/US99/03826
15 PRIOR FILING DATE: 1999-02-22
16 NUMBER OF SEQ ID NOS: 87
17 SOFTWARE: FastSeq for Windows Version 4.0

```

SEQ ID NO 27
LENGTH: 389
TYPE: PRT
ORGANISM: H. sapiens
US-09-336-643A-27

Query Match 8.6%; Score 153.5; DB 4; Length 389;
Best Local Similarity 34.3%; Pred. No. 5e-07;
Matches 49; Conservative 21; Mismatches 58; Indels 15; Gaps 6;

QY 108 RODGAMSSDAEDDELPAPATQAGHALPLPOEPPEVPLINGAHFTTLSTLCY 167
DB 57 RDDDVLCVCCGE-PEIDPQDTSKPEG-----LIGFHDMLTLVNGRYFTTSTLVNK 110
QY 168 E-DTMLAAMF--SGRHYPIDSGRYFIDRDGTHFGDVLNLSGDLPPRRVR--AYYK 222
DB 111 EPMSTLHMKKQVWGNKODHRCALIDRSPEYFEPILNLRGQLVNDGINLGYLE 170
QY 223 EAQYATGPLEOLE---NMQP 241
DB 171 EARFPGIDSLIHEHVAIKNSQP 193

RESULT 6
US-08-606-143-44
Sequence 44, Application US/08606143
Patent No. 5856155

GENERAL INFORMATION:
APPLICANT: LI, MIN
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John

REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
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TELEFAX: (312) 616-5700
TELEX: 25-3533

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-44

Query Match 7.8%; Score 138; DB 2; Length 162;
Best Local Similarity 37.3%; Pred. No. 4.6e-06;
Matches 41; Conservative 19; Mismatches 45; Indels 22; Gaps 4;

QY 146 EYVPLINGAHFTTLSTLCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDVLNF 205
DB 2 EYLVVNSGRFEPWKNLTDRYPTLLGS--SEKEFFDAESGEYFDRDPMFRHYLNF 59

QY 206 LNSGDL--PPRRVRVAYKEAQAIGPLLEQ---LENNQPLGKGRVQALIMPYKRD 260
DB 60 YATGRHCHRCQICQAFDELAIFYGLVPELVGCCLEFRDRK-----KE 104
QY 261 HIERIVE 267
DB 105 NAERLAE 111

RESULT 7
US-09-336-643A-10
Sequence 10, Application US/09336643A
Patent No. 6399761

GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutler, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1998-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10

LENGTH: 646
TYPE: PRT
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(646)
OTHER INFORMATION: Xaa - Any Amino Acid
US-09-336-643A-10

Query Match 7.5%; Score 133.5; DB 4; Length 646;
Best Local Similarity 29.9%; Pred. No. 0.00011;
Matches 44; Conservative 19; Mismatches 51; Indels 33; Gaps 5;

QY 137 LPLPQEP-----EYVPLINGAHFTTLSTLCYEDTMLAAMFSGRHYIPTD 185
DB 20 LPPAQOPLPAPGVKASRGDXVLVNVSGRRFETWKNLTDRYPTLLGS--SEKEFFYDA 77

QY 186 SEGRYFIDRDGTHFGDVLNLSGDL--PPRRVRVAYKEAQAIGPLLEQ---LENNQ 240
DB 78 DSGRYFIDRDGTHFGDVLNLSGDL--PPRRVRVAYKEAQAIGPLLEQ---LENNQ 137

QY 241 PLKGRVROAFLGIMPYKDLIERIVE 267
DB 138 DRK-----KENAERLAE 149

RESULT 8
US-09-142-791A-2
Sequence 2, Application US/09142791A
Patent No. 6368823

GENERAL INFORMATION:
APPLICANT: Antoine Michel Alain Brill
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Fatvre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rounet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02

RESULT 12
US-09-142-791A-6
; Sequence 6, Application US/09142791A
; Patent No. 6368823

GENERAL INFORMATION:
APPLICANT: Antoine Michel Alain Brill
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Falvay
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rounnet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 636
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-142-791A-6

Query Match 6.7%; Score 120; DB 4; Length 636;
Best Local Similarity 27.0%; Pred. No. 0.0023;
Matches 40; Conservative 22; Mismatches 44; Indels 42; Gaps 6;

QY 137 LPLP---QEPVVPVPLNIGAHFTTSLTLCYEDTMLAMFSGNHYIPTDSGRYFI 192
DB 27 MPLAPADKNRODELLIYANSGRRFTWRTTLERYPTLLGS--TEKEFFENEDTKEYFF 84
QY 193 DRDGTGHDVNLNLSGSDLPERRRVRVYKQAYATGPLENNQPLKGEVROAFL 252
DB 85 DRDPEVFRCLVNYFRGKL-----HYTRKICISAYDEL-----AFY 121
QY 253 GLMP-----YKRD-----HLRIYE 267
DB 122 GILPEITIGDCYEYKDRKRENERLMD 149

RESULT 13
US-08-606-143-45
Sequence 45, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: LI, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
NUMBER OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-45

Query Match 6.7%; Score 119.5; DB 2; Length 159;
Best Local Similarity 28.7%; Pred. No. 0.00031;
Matches 39; Conservative 14; Mismatches 44; Indels 39; Gaps 4;

QY 147 VPLNIGAHFTTSLTLCYEDTMLAMFSGNHYIPTDSGRYFI DRDGTGHDVNL 206
DB 3 LILVNSGTRFQWDTLERYPTLLGS--SERDEFYHBTQOYFDRDPDIRHILNFX 60
QY 207 RSGDLPERRRVRVYKQAYATGPLENNQPLKGEVROAFLGLMP-----Y 257
DB 61 RGLHYPHRCISAYDE-----ELAFGLPEITIGDCYEE 96
QY 258 YKD---HLRIYE 269
DB 97 YKDRRENERLMD 112

RESULT 14
US-08-470-335-188
Sequence 188, Application US/08470335F
Patent No. 6147190
GENERAL INFORMATION:
APPLICANT: GOODEARL, ANDREW
APPLICANT: STROOBART, PAUL
APPLICANT: MINGHETTI, LUISA
APPLICANT: WATERFIELD, MICHAEL
APPLICANT: MARCHIONNI, MARK
APPLICANT: CHEN, MARIO S.
APPLICANT: HILES, IAN
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
TITLE OF INVENTION: PREPARATION AND USE
FILE REFERENCE: 04585/00200B
CURRENT APPLICATION NUMBER: US/08/470,335F
CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/036,555
EARLIER FILING DATE: 1993-03-24
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 188
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-08-470-335-188

Query Match 6.1%; Score 108.5; DB 4; Length 349;
Best Local Similarity 23.5%; Pred. No. 0.013;
Matches 70; Conservative 33; Mismatches 98; Indels 97; Gaps 14;

QY 9 RKGGRGRLRRPLA-----LPALRLGELPANOGSTASASGGRSGRGAOPAGRERGV 61
DB 9 RGRGRGRLRRGSRASRSPPLPLPLLLL-----GTALLAPAAAGNEAAPG----- 58
QY 62 EGATLPPAHCHSPBSGQAPAGRVMPGAARRANGMYVYVGRPDSRQDAMS----- 114
DB 59 -----ASVCYSSP-----BSVGSVDELAQRAA---VVEGKVPDROROCALRKAAAAA 105
QY 115 -----SSDAEDDFLE-----PATPAT-----QAGHALPLPOEF 144
DB 106 GAGANGGRERPPAOPRALGPPAEPLLAANGTVSWPTAPVPSAGCEPEAEAYL-VKV 164

```

Oy 145 PEVPLNMG---AHFTTRJSTLRCEYEDMLAMEGRRHPT-----DSEGRYIDR 194
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 165 HQWAVYAGGAKKNSLTLYAGTM-----GHAPSPCGRLKEDSRIFEMEP 211
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 195 DGHFGDVLNLRSGDLPREPRNAYKKE-----AQYRGLPLEOLENNOPLKGEV 247
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 212 DANSTRAAPAAPFR-SPPLETGHNLRKESRYLCKKCALPRLKEMKSOASAGSKL 268

```

RESULT 15
US-08-467-602-382

; Sequence 382, Application US/08467602C
; Patent No. 6444642
; CURRENT INVENTOR

; GENERAL INFORMATION:
: APPLICANT: sklar E

```

; APPLICANT: Sklar, Robert
; APPLICANT: Marchionni, Mark

```

APPLICANT: Gwynne, David I.

; TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND
; TITLE OF INVENTION: DISORDERS
;

CURRENT APPLICATION NUMBER: US/08/467,602C

CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/209-204

EARLIER FILING DATE: 1994-03-08

EARLIER APPLICATION NUMBER: 08/059,022
EARLIER FILING DATE: 1993-05-06

NUMBER OF SEQ ID NOS: 420

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; SOFTWARE: FastSEQ for Windows V
: SEQ ID NO 382

```

LENGTH: 382

TYPE: PRT
ORGANISM: F

FEATURE:

NAME/KEY: V
LOCATION:

OTHER INFORMATION: Xaa

US-08-467-602-3

Query Match

Best Local Similarity
Matches 70: Consensus

100-443897-1

QY 9 RKGKGE

Query Match	6.18; Score 108.5; DB 4; Length 382;
-------------	--------------------------------------

```

QY 9 RKKGQJLRRPPL-----LPLRLRGJLPANOGYSAASASSGRSGQAPGRERGV 61
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 43 RSGRRPQAQRGSAANSSPLPLPLLLLL-----GTRALAPGAANEAPAG----- 92
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 62 EGATLPAHCLSPSPQAPAGRWPGARAGMYYVTGREGPSRQDGMS----- 114
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 93 -----ASVYSSP-----PSVGSVOELAORA-----VIEGVHVEPRROOQGLRKAATA 139
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 115 -----SSDEDDFILE-----PATPAT-----OAGHALDPLQEF 144
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 140 GEGAMGQDREPPAPAGPAPALCPPEEPLIANGTVSPFPIAPVSAGEPGEAPYL-VKV 198
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 145 PEVYPLNTG-----AHFTRLSTJRCYEDTLMAMFSGRHYIP-----DSEGRYIDR 194
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 199 HQWAVKAGAGLKKDLSILTVLRGTW-----GHPAFPCGRUKEDRSRYIFMEP 245
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 195 DCTHGDVTLNLRSDLLPRRERYAYKE-----AQYIAIGPLLEJLENNQPLKGEV 247
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 246 DANSTRAPAAPRA-SPEPLTGRUKKEYSVLCKRCALPRLKKNKSQSAAGSL 302
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: February 12, 2003, 11:09:23
Job time : 18 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:04:55 / Search time 14 Seconds

(without alignments)
1016.170 Million cell updates/sec

Title: US-10-086-156-24

Perfect score: 1780
Sequence: 1 MTMAVLRNRKRGKGLRRRRP.....NNEKKSPVQLPAGVFQHFNG 343

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	175	9.8	316	TNPL_HUMAN	Q13829 homo sapien
2	151	8.5	265	Y176_HUMAN	Q14681 homo sapien
3	123	6.9	460	MYCN_MARMO	Q61976 marmota mon
4	122.5	6.9	601	CIR5_MUSPF	P79197 mustela put
5	121	6.8	490	CIRL_DROME	P17971 drosophila
6	121	6.8	602	CIR5_MOUSE	Q61762 mus musculu
7	119.5	6.7	613	CIR5_HUMAN	P22460 homo sapien
8	113.5	6.4	602	CIR5_RAT	P19024 rattus norv
9	112	6.3	2517	NCR2_HUMAN	Q9Y618 h nuclear r
10	110	6.2	598	CIR5_RABIT	P50638 corycolagus
11	106.5	6.0	525	CIR3_RAT	P15384 rattus norv
12	106.5	6.0	656	CIR5_DROME	P08510 drosophila
13	105.5	5.9	464	MYCN_HUMAN	P04198 homo sapien
14	105.5	5.9	825	SE5_RAT	O63003 rattus norv
15	105	5.9	499	CIR5_HUMAN	P16389 homo sapien
16	104.5	5.9	985	CIRK_DROME	P17970 drosophila
17	103.5	5.8	757	CIRK_MOUSE	Q14003 homo sapien
18	101.5	5.7	294	NTG5_MOUSE	O08600 mus musculu
19	101	5.7	499	CIRK_MOUSE	P15386 mus musculu
20	101	5.7	528	CIRK_MOUSE	P16389 mus musculu
21	101	5.7	740	GAG_SMRVH	P121411 squitrel mo
22	101	5.7	960	EGDI_MOUSE	P52734 mus musculu
23	100.5	5.6	523	CIR3_HUMAN	P22001 homo sapien
24	100.5	5.6	1319	MNL_HUMAN	Q10571 homo sapien
25	100	5.6	493	CIRK_MOUSE	P16388 mus musculu
26	100	5.6	495	CIRK_MOUSE	P10499 rattus norv
27	100	5.6	1411	TCOF_HUMAN	P13448 homo sapien
28	99	5.5	495	CIRK_HUMAN	O09470 homo sapien
29	98	5.5	356	Y429_HUMAN	O43312 homo sapien
30	98	5.5	961	EGDI_HUMAN	P98174 homo sapien
31	97	5.4	499	CIR2_XENTIA	P22739 xenopus lae
32	97	5.4	960	SMC_RAT	Q9W13 rattus norv
33	97	5.4	993	ROXN_HUMAN	Q9UG12 homo sapien

ALIGNMENTS

RESULT 1	ID	TNPL_HUMAN	STANDARD	PRT	316 AA.
AC	Q13829				
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Tumor necrosis factor, alpha-induced protein 1, endothelial (B12 protein)				
GN	TNFAIP1 OR EDPI.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-Endothelial cells;				
RX	MEDLINE-92112779; PubMed-1370465;				
RA	Wolf F.W., Marks R.M., Sarma V., Byers M.G., Katz R.W., Shows T.B., Dixit V.M.;				
RT	"Characterization of a novel tumor necrosis factor-alpha-induced endothelial primary response gene."				
RL	J. Biol. Chem. 267:1317-1326(1992).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-Lung;				
RA	Strausberg R.;				
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.				
CC	- INDUCTION: BY TNF-ALPHA, INTERLEUKIN-1 BETA AND LIPOPOLYSACCHARIDE (LPS)				
CC	- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).				
CC	EMBL: M80783; AAA58385.1; -				
DR	EMBL: AY065346; AAL38649.1; -				
DR	EMBL: BC001643; AAH01643.1; -				
DR	EMBL: BC001949; AAH01949.1; -				
DR	Genew; HGNC:11894; TNFAIP1.				
DR	MIM: 191161; -				
DR	InterPro: IPR000210; BTB_POZ.				
DR	InterPro: IPR003131; Ktetra.				
DR	Pfam: PF02214; Ktetra; 1.				
DR	SMART; SM00225; BTB; 1.				
DR	PROSITE; PS50097; BTB; 1.				

FT	DOKAIN	28		96	B.T.B.
SQ	SEQUENCE	316 AA;	36204 MW; D20B810A00507DCF CRC64;		
	Query Match		9.88; Score 175; DB 1:	Length 316;	
	Best Local Similarity	37.98;	Pred. No. 1.2e-05;		
	Matches 47;	Conservative 23;	Mismatches 48;	Indels 6;	Gaps 5;
OY	148 VPLNIGAHETRLSTLCYCIEDTMIAMFSGRHVPTDSEGRFITRDGTGEGDVLFNR	207			
	: : : : : : : : : : : : : : : : :				
Db	30 VOLNVAGSLYYTTVRALRNL-DTMKMAFGSMEVLTPTEKEGILLDRCKGNHGGTILNYLR	88			
OY	208 SG--DLPP-RERVARAVYEAKOYAVALGPLEELEN-MQLKGKERQAQAFGLMPYYKDHL	263			
	: : : : : : : : : : : : : : : : :				
Db	89 DDITLPGNQREIKELMAREAYYLLOGLVNNGQSALDQKNDSYGVCNPITLSKEE-E	147			
OY	264 RIVE	267			
	: : :				
Db	148 RLIE	151			

```

RESULT 2
Y176_HUMAN
ID Y176_HUMAN STANDARD; PRT; 265 AA.
AC Q14681;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein KIAA0176 (Fragment).
GN KIAA0176.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RF TISSUE-Bone marrow.
RX MEDLINE=96281124; PubMed=8724849;
RA Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. V.
RT The coding sequences of 40 new genes (KIAA0151-KIAA0200) deduced by
RT analysis of cDNA clones from human cell line KG-1."
RL DNA Res. 3:17-24(1996).
CC -1- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC -----
CC CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC -----
CC EMBL: D79998; BA011493.1; -.
CC DR InterPro: IPR000210; BTB_POZ.
CC DR InterPro: IPR001311; K_tetra.
CC DR Pfam: PF02214; K_tetra; 1.
CC DR SMART: SM00225; BTB; 1.
CC DR PROSITE: PSS0097; BTB; FALSE_NEG.
CC KM Hypothetical protein.
CC FT NON_TER 1
CC FT DOMAIN 74 174 BTB
SQ SEQUENCE 265 AA; 28801 MW; 5C7455CCBBE8924 CRC64;
Query March 8.5%; Score 151; DB 1; Length 265;
Best local similarity 25.0%; Pred. No. 0.0005;
Matches 73; Conservative 26; Mismatches 95; Indels 98; Gaps 14;
QY 26 LRLGELPANOGTSAASASGRRSGQADPGRERGVGEGATLPPAHCLSP-PSGQPAAGR 84
DB 6 LQLDPAWAGLG-----GGGSGVGDGCGP-----VRC-----PP-----SPRAPGTPRGH 46
QY 85 VMPGARARARQMYVTGTGEPDPSRKDDGMSSDAEDDLELATPATQAGHRLPLPDEF 144

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Dd      47 GRPAAA-----VAQRLPEG-----PGPPERAGGGGA-----72
OY      145 PEVYPVLINGCAHEPTTRUSTLR-----CYETMLAMFSGRAHYIPTDSEGRYEID    193
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       73 ARWRLANNGGYEFTTROTTLREPKSFCLRCCDEDELDS-----DKDETGAFLID    144
OY      194 RDGTGHGEGVYNLEASSGLPPRRERY--RAYVKENQVYAIGPLELENNOPLUKEKRVQAQ    251
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       125 RDPFYFGILNLYLRHGKLITLKEELAEGBGVLEAEAFYNIASIVR-----LVKERIR--    174
OY      252 LGLMPYYCDHLER-----IYEIARLARAVQRARAKLSLTSPWLMSVLIKM    298
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       175 -----DNENRTSGGPRKYKVYINVLQQCEBELTQMSTYSMDGKTFQLLI    218
```

ID	MYCN_MARMO	STANDARD;	PRT;	460 AA.
AC	061976;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	N-myc proto-oncogene protein (N-mycl).			
OS	MYCN OR NMYC OR NMYC1.			
OC	Marmota monax (Woodchuck).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;			
OC	Marmota.			
OX	NCBI_TaxID=9995;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RC	MEDLINE=90370481; PubMed=2395655;			
RA	Fourel G., Tjollais P., Brienda M.-A.,			
RL	"Nucleotide sequence of the woodchuck N-myc gene (WN-mycl).";			
CC	Nucleic Acids Res. 18:918-918(1990).			
CC	-1 SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER			
CC	BHLH PROTEIN. BINDS DNA AS AN HETERODIMER WITH MAX.			
CC	-1 SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF			
CC	TRANSCRIPTION FACTORS. BHLH-ZIP SUPERFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X53673; CAA37712.1; .			
DR	EMBL; X53674; CAA37712.1; JOINED.			
DR	HSSP; P25912; HLDO.			
DR	TRANSFAC; T03440; .			
DR	InterPro; IPR001092; HLH_Basic.			
DR	Interpro; IPR002418; TF_MYC.			
DR	pfam; PF000010; HLH_1.			
DR	pfam; PF01056; MYC_N-term; 1.			
DR	PRINTS; PR00044; LEVZIPRMYC.			
DR	SMART; SM00353; HLH_1.			
DR	PROSITE; PS00038; HLH_1; 1.			
DR	PROSITE; PS50888; HLH_2; 1.			
KW	Nuclear protein; DNA-binding; Proto-oncogene; Phosphorylation.			
FT	DOMAIN 258 274			
FT	DNA_BIND 377 390			
FT	DOMAIN 391 430			
FT	DOMAIN 429 450			
FT	MOD_RES 257 257.			
FT	MOD_RES 257 257.			
FT	MOD_RES 259 259			
FT	SEQUENCE 460 AA; 49192 MW; 8A16686C82FFB02E CRC64;			
FT	(BY SIMILARITY)			
FT	(BY CK2)			
FT	PHOSPHORYLATION (BY CK2)			
FT	(BY SIMILARITY)			
FT	ASP/GLU-RICH (ACIDIC).			
FT	BASIC DOMAIN.			
FT	HELIx-LoOp-HELIx MoTIF (By SiMiLaRiTy).			
FT	LEUCINE-zIPPER (PoTeNTIAl).			
FT	PHOSPHORYLATION (By CK2)			
FT	(By SiMiLaRiTy).			
FT	PHOSPHORYLATION (By CK2)			
FT	(By SiMiLaRiTy)			

Query Match 6.9% Score 123; DB 1; Length 460;

Best Local Similarity 19.9%; Pred. No. 0.097;
Matches 69; Conservative 48; Mismatches 115; Indels 114; Gaps 14;

QY 4 AVLRNRKGGKGLRRRLPALRLGELPANOGCTSAASASRRSGQAPRRERGVEG 63
DB 130 AVSEKQHRGRP-----PAAAGPA-----TPGAGAAANAGCHGTAGAGGALLPA 176
QY 64 AVALPPHCLSP-----PSGPPAAGVHMGGAARRAGMYV-----VT 100
DB 177 ELAHPAAECVDVAVPPFVNKDPAPVPAPAGSAPVGAAGAAPASAAVAPPRIG 236
QY 101 GDEPD-----SRDDGAMSSSDADDEFLP-----ATPTAQGHALPL 140
DB 237 GPPANGGDHAKALSTSGEDPLSDDEDEDEEEDVYTVKRRSSSKAVTFTTIT 296
QY 141 PDEPPVPLNIGGAHFTTRLRCYEDTMLAAMPGRHYIPDSGRFYIDRDGTHFG 200
DB 297 VR--FKNALGIGRAO--SEELIKRC-----VPHOHNTPASP----- 333
QY 201 DVALNFLRSGDLPPRRERAVYKRAOYTAIGPLLEOLENMOPLGK----- 246
DB 334 -----YVESDAPQKIKSVSPRLKSVIP--PKAKSLSPNDSDESRHNNILIR 387
QY 247 -----VROAFGLMPYKDKHLEIVEIARAVOKRAFKLSLT 287
DB 388 ORRNDLRSSFLTL-----RDHVPFLYK-----NEKAKVYLKKRAT 423

RESULT 4
ID CIK5_MUSPF STANDARD; PRT; 601 AA.
AC P79197;
DT 30-MAY-2000 (rel. 39, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE Voltage-gated potassium channel protein Kv1.5.
GN KCNA5.
OS Musceta putorius furo (Ferret).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Musceta.
OX NCBI_TaxID=9669;
[1]
RP SEQUENCE FROM N.A.
RC Tissue=Heart atrium;
RL Schlegel T., Polander K., Swanson R.;
Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CONFORMATION, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
GRADIENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
EVERY THIRD POSITION.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
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or send an email to license@ebi.ac.uk).
CC EMBL; U45979; AAB4145.1; -

DR HSP; Q54397; 1BL8.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR001622; K+-channel_pore.
DR InterPro; IPR004052; KV15channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR000636; M+-channel_nlg.
DR InterPro; IPR003972; Shaker_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01512; KV15CHANNEL.
DR PRINTS; PR01491; KCHANNEL.
DR PRINTS; PR01496; SHAKERCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 240 258
FT TRANSMEM 314 334
FT TRANSMEM 345 366
FT TRANSMEM 386 407
FT TRANSMEM 422 443
FT TRANSMEM 483 504
FT DOMAIN 370 375
FT CARBOHYD 114 114
FT CARBOHYD 179 179
FT CARBOHYD 288 288
SQ SEQUENCE 601 AA; 65889 MW; 142DB98CB43FE0 CRC64;

Query Match 6.9%; Score 122.5; DB 1; Length 601;
Best Local Similarity 23.8%; Pred. No. 0.15;
Matches 81; Conservative 39; Mismatches 148; Indels 73; Gaps 17;

QY 26 LRLGELPANOGCTSAASASRRSGQAPRRERGVEGATLPPACLSPPSGQAPAGRY 85
DB 1 MEIALVPLENGD-----AMTVRGGEAGTGCSD--ALGELQCPPLAGLSGPREPAP-- 51
QY 86 MGAARBARNGMYVNGREDSRRDAMSSSDADDEFLP--APPTAQGHALPLPQEF 144
DB 52 -----RANG-----TORGVD-----PGRPPLPPLPQPPQRRRLPPEDEBEGPALMAE 97
QY 145 PEV-----VPLNIGAHFTTRLSTLCYEDTMLAAMFSG--RHYPIDSEGRYFD 193
DB 98 DQVLGAGSLHQRLVNLINISGLRFTQGLAQPPNLLGDPAKRLRFQPLRNE--YFFD 155
QY 194 RGTGHRGDVLANLRSGD---LPPRRERAVYKRAOYTAIG-PLLEQL-----ENMOP 241
DB 156 RRPSPFDGLYYOOSGRRLRPVNSLDVFADEIRRYQLDEAMERREDEGFIKEEKP 215
QY 242 L-KGEVROAFGLMPYKDKHLEIVEIARAVOKRAFKLSLTPSWLMVYLKMP 300
DB 216 LPRNERQOVWL-----ITEYPPSSSANGIALVSVLVILITTCLETLPE 263
QY 301 GVTSWINAEERLYLETPI-----GPERONNEKSPVOLPAG 336
DB 264 -----FRDERELLRHPPVPVHPQPLGPRGAN--GSGPLAPPSG 298

RESULT 5
ID CIKL_DROME STANDARD; PRT; 490 AA.
AC P17971; Q9VW11;
DT 01-NOV-1990 (rel. 16, Created)
DT 01-NOV-1990 (rel. 16, Last sequence update)
DT 01-JUN-2002 (rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein Shal (Shal2).
GN SHAL OR SHAL2 OR CG9262.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90239553; PubMed-2333511;
 RA Wel A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "K+ current diversity is produced by an extended gene family
 conserved in Drosophila and mouse."
 RL Science 248:599-603(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90245668; PubMed-2336395;
 RA Wel A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "Shal, Shab, and Shaw: three genes encoding potassium channels in
 Drosophila."
 RL Nucleic Acids Res. 18:2173-2174(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blake J.R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
 RA Butts K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dong L.E., Downes M., Dugan-Rocha S., Dunkov B., Eltschman W.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hristova M., Houston K.A., Howland T.J., Wei M.-H., Ibegwu C.,
 RA Jaiswal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel P.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mestrovic G., Milshina N.V., Mobarry C., Morris J., Moshire A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pauley J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui Y., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 GRADIENT. MAY PLAY A ROLE IN THE NERVOUS SYSTEM AND IN THE
 REGULATION OF BEATING FREQUENCY IN PACEMAKER CELLS.
 CC -1- SUBUNIT: HETEROOTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT

CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CC CURRENT CLASS.
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC -----
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 CC -----
 DR EMBL: M32660; AAA28895.1; ALT_SEQ.
 DR EMBL: AE003516; AA069144.1; ALT_SEQ.
 DR PIR: A35312; A35312.
 DR PIR: S12747; S12747.
 DR Flybase: FBgn0005564; Shal.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K-channel_pore.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR003968; K_channel.
 DR InterPro: IPR000636; M-channel_nlg.
 DR InterPro: IPR003975; Shal_channel.
 DR Pfam: PF00520; Ion_trans_1.
 DR Pfam: PF02214; K_tetra_1.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR01491; KCHANNEL.
 DR PRINTS: PR01497; SHALCHANNEL.
 DR SMART: SM00225; BTB_1.
 DR SMART: SM00225; BTB_1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Alternative splicing.
 FT TRANSMEM 186 204 SEGMENT S1.
 FT TRANSMEM 229 250 SEGMENT S2.
 FT TRANSMEM 261 282 SEGMENT S3.
 FT TRANSMEM 290 308 SEGMENT S4.
 FT TRANSMEM 324 345 SEGMENT S5.
 FT TRANSMEM 385 406 SEGMENT S6.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 490 AA; 55918 MW; E178ELC89B07DA74 CRC64;
 Query Match 6.8%; Score 121; DB 1; Length 490;
 Best Local Similarity 27.0%; Pred. No. 0.15;
 Matches 41; Conservative 17; Mismatches 46; Indels 46; Gaps 6;
 QY 128 PTAQAGALPLPLPEP-----EYPLNIGAHFTTRSLRCYEDTMIAMFSGR 179
 DB 20 PIATH-----PIPPPMKRRRTDKLLINVSGRFETWNTLEKYDITLGS--NR 72
 QY 180 HYPTDSGRFYIDGTHFVDVLFNLGSLP-PRERVAYVKEAQYVAIGPLLEQLN 238
 DB 73 EFTDECKEFTFDPDPIFRILINYYRKGKLYRKHCELTSTDE----- 117
 QY 239 MQLPKERYQAFGLMP-----YKDHLE 264
 DB 118 -----ELAFGLMDVLDCCYEDYDR 140
 RESULT 6
 CIRC_MOUSE
 ID CIRC_MOUSE STANDARD; PRT; 602 AA.
 AC 061762;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Kv1.5 (Kv1.5).
 GN KCNA5.
 OS Mus musculus (Mouse).

FT MOD_RIST 557 557 PHOSPHORYLATION (BY PKA) (POTENTIAL).
FT CONFLICT 55 55 MISSING (IN REF. 1).
FT CONFLICT 138 138 L -> Q (IN REF. 2).
FT CONFLICT 154 154 P -> R (IN REF. 3).
FT CONFLICT 187 188 R -> G (IN REF. 1).
FT CONFLICT 214 214 R -> G (IN REF. 2).
FT CONFLICT 228 228 P -> V (IN REF. 2).
FT CONFLICT 282 282 L -> V (IN REF. 3).
FT CONFLICT 307 307 P -> A (IN REF. 1).
FT CONFLICT 579 613 GSCLECNVAKSNVDRSLALCDTSHETDL ->
FT SEQUENCE 613 AA; 67168 MM; 65324F04P127C5BC CRC64;
FT
SQ
Query Match 6.7%; Score 119.5; DB 1; Length 613;
Best Local Similarity 22.5%; Pred. No. 0.24;
Matches 62; Conservative 27; Mismatches 101; Indels 85; Gaps 11;
QY 26 LRLGELPANGCGTSAASASGSRGSGQAVARGRVEGATLAPNAHCSPSSGQPA-AGR 84
DB 1 KEIALIVPLENGAMTVKRGDGNKACGGA-----TGSELQCPAGLSDGKPEAPKGR 54
QY 85 VMPGARARAGMVTYTGHPDSRRDGMSSSDADDLEPATPYATGALPLLPQEF 144
DB 55 ---GAGRA-----DSEVRPLPLPDGCVPLPLPEL 85
QY 145 P-----EVPNLGGAHFTTRLSTLRCEYDTM 171
DB 86 PRPRPPDEDEEEDGPDGLGVEDQALSTALHQRVHNINSIGLRFETQLGIAQFPWTL 145
QY 172 LAAMSGSHYI-PIDSEGRYFIDRGCTHFQVLYNLBRGD---LPRRVRAYIKYAOY 227
DB 146 LGDPARKLPLYPDLPLNE--YFDNRNPSFDGLTYGGGRLRPVNSLDVFADEIRFY 203
QY 228 AIG-PLLEQL-----ENMQPL-KGKVRQAF 252
DB 204 QLGDEAMERFDEDFIKEEKPLPRNFQWYL 238
RESULT 8
CIR5_RAT STANDARD; PRT: 602 AA.
AC CIR5_RAT STANDARD; PRT: 602 AA.
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein Kv1.5 (Kv1) (RCK7).
GN KCMAS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_Taxid:10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain.
RX MEDLINE-90297965; PubMed-2361015;
RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
RA Foldander K., Luneau C.J., Antkowiak J., Oliva C., Buhrow S.A.,
RA Bennett C., Stein R.B., Kaczmarek L.M.;
RT "Cloning and expression of cDNA and genomic clones encoding three
RT delayed rectifier potassium channels in rat brain.";
RL Neuron 4:929-939(1990).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- DOMAIN: THE SEGMENT 54 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.

CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SMRT/TRAC-2 (SHOWN HERE) AND
 CC TRAC-1; ARE PRODUCED BY ALTERNATIVE SPLICING. TRAC-1 CONTAINS ONLY
 CC THE C-TERMINAL RECEPTOR-INTERACTING DOMAIN AND ACTS AS AN
 CC ANTI-REPRESSOR.
 CC -1- TISSUE SPECIFICITY: UBQUITOUS. HIGH LEVELS OF EXPRESSION ARE
 CC DETECTED IN LUNG, SPLEEN AND BRAIN.
 CC -1- INDUCTION: REGULATED DURING CELL CYCLE PROGRESSION.
 CC -1- DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT
 CC ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RD1, RD2
 CC AND RD3). THE C-TERMINAL REGION CONTAINS THE NUCLEAR RECEPTOR-
 CC INTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION
 CC DOMAINS (ID1 AND ID2).
 CC -1- DOMAIN: THE TWO INTERACTION DOMAINS (ID) CONTAIN A CONSERVED
 CC SEQUENCE REFERRED TO AS THE CORN BOX. THIS MOTIF IS REQUIRED AND
 CC SUFFICIENT TO PERMIT BINDING TO UNLIGANDED TR AND RARS SEQUENCES
 CC FLANKING THE CORN BOX DETERMINE NUCLEAR HORMONE RECEPTOR
 CC SPECIFICITY.
 CC -1- SIMILARITY: CONTAINS 1 SANT-A DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF113003; AAD20946.1; -
 DR EMBL: AF125672; AAD22973.1; -
 DR EMBL: U37146; AAC50236.1; -
 DR EMBL: S83390; AAB50847.1; -
 DR EMBL: U80750; AAB91446.1; -
 DR TRANSFAC: T04689; -
 DR Genev: HGNC:7673; NCOR2.
 DR MIM: 600848; -
 DR InterPro: IPR001005; MYB_DNA_binding.
 DR Pfam: PF00249; MYB_DNA-binding; 2.
 DR SMART: SM00395; SANT; 2.
 DR PROSITE: PS50090; MYB_3; 1.
 KW Nuclear protein; Transcription regulation; DNA-binding; Repressor;
 KW Coiled coil; Alternative splicing.
 FT DOMAIN 174 215 COILED COIL (POTENTIAL).
 FT DOMAIN 254 312 INTERACTION WITH SIN3A/B (BY SIMILARITY).
 FT DNA_BIND 429 474 SANT-A (POTENTIAL).
 FT MYB 613 657 MYB.
 FT DOMAIN 522 561 COILED COIL (POTENTIAL).
 FT DOMAIN 778 820 PRO-RICH.
 FT DOMAIN 2139 2143 CORN BOX OF ID1.
 FT DOMAIN 2342 2346 CORN BOX OF ID2.
 FT DOMAIN 494 510 POLY-GLN.
 FT DOMAIN 682 685 POLY-LYS.
 FT DOMAIN 994 1002 POLY-PRO.
 FT DOMAIN 1384 1389 POLY-PRO.
 FT DOMAIN 1842 1846 POLY-GLY.
 FT DOMAIN 2479 2482 POLY-PRO.
 FT VARSPLIC 1 1702 MISSING (IN ISOFORM TRAC-1).
 FT VARSPLIC 2353 2398 MISSING (IN ISOFORM TRAC-1).
 FT CONFLICT 7 7 L -> P (IN REF. 2).
 FT CONFLICT 295 295 K -> E (IN REF. 2).
 FT CONFLICT 309 309 L -> W (IN REF. 2).
 FT CONFLICT 352 352 MISSING (IN REF. 2).
 FT CONFLICT 365 365 A -> P (IN REF. 2).
 FT CONFLICT 612 613 SS -> EF (IN REF. 5).
 FT CONFLICT 711 711 S -> T (IN REF. 2).
 FT CONFLICT 724 740 MISSING (IN REF. 2).
 FT CONFLICT 787 796 BTRAPREP -> PEDIPAPES (IN REF. 2).
 FT CONFLICT 804 804 G -> L (IN REF. 2).
 FT CONFLICT 814 814 S -> F (IN REF. 2).

FT CONFLICT 817 817 A -> S (IN REF. 2).
 FT CONFLICT 889 889 G -> R (IN REF. 2).
 FT CONFLICT 1023 1030 SRPAPPA -> MEAMPAP (IN REF. 3).
 FT CONFLICT 1034 1034 A -> AEKPYEPA (IN REF. 2).
 FT CONFLICT 1894 1894 K -> T (IN REF. 4).
 FT CONFLICT 2494 2494 P -> A (IN REF. 4).
 SQ SEQUENCE 2517 AA; 274031 MW; F5805C01761258C0 CRC64;
 Query Match 6.3%; Score 112; DB 1; Length 2517;
 Best local similarity 21.9%; Pred. No. 4.6;
 Matches 68; Conservative 23; Mismatches 104; Indels 116; Gaps 12;
 QY 15 PLRRRLPALRLG-ELPANOGTSAASASSGRRSGCAPARRVGEATAPANCL 73
 DB 1440 PLAPRLKESINOGTGLKDYTGASTGSKKHVRS-----LIGSGRT-PPVAPL 1490
 QY 74 SPSSGCPAAGV-----MPGAARRAGNV----- 98
 DB 1491 DVADARALRACYEESLKSHPGTAASSGSIAGAPVYELKPRGSPPLYEDHGAFF 1550
 QY 99 -----VTGREPDSRRDGDANSSSDAEDDFLEPAP-----TATQAGHALPLP 141
 DB 1551 AGHLPRGSPYTMREPTRLQSGSLSSSKASQDRKLTSPRIAKSPHSTVEHHHPISP 1610
 QY 142 QE-----PEVYVPLNIGAHFTTRLST-----L 164
 DB 1611 YEHILRGVSGVDYLRSHIPLAFDPTISPRGIPDLAAAYVLRPHLAPNTPYPLI 1670
 QY 165 RCYEDTMAMFSGRHIIPTDSEGRYFDRCGTDFGVDLNLBSGD-----LPPRRVNAV 220
 DB 1671 RGPVDT---VALENKQITIND-----YITSCQMHNTATMAORADMLRGLSPRESSIAL 1722
 QY 221 YKEAOYTAIGP 231
 DB 1723 -----NYTAGP 1728
 RESULT 10
 CITS_RABIT STANDARD; PRT; 598 AA.
 AC P50638;
 NC 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Voltage-gated potassium channel protein Kv1.5.
 GN KCNA5.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 OX [1]
 RP SEQUENCE FROM N.A.
 RP SPRAIN-Japanese white; Tissue-Heart;
 RC MEDLINE=96032538; Pubmed=755635;
 RX Sasaki Y., Ishii K., Nunoki K., Yamagishi T., Taira N.,
 RT "The voltage-dependent K⁺ channel (Kv1.5) cloned from rabbit heart
 RT and facilitation of inactivation of the delayed rectifier current by
 RT the rat beta subunit".
 RL FEBS Lett. 372:20-24(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP SPRAIN-New Zealand white; Tissue-Portal vein;
 RC Clement-Choulemme O., Ishii K., Walsh M.P., Cole W.C.;
 RT "Rabbit portal vein Kv1.5".
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RP Tissue-Smooth muscle;
 RC Tate R.J., Osipenko O.N., Kempall F.E.J., Gurney A.M.;
 RT "Identification of a voltage-gated potassium channel (Kv1.5) in rabbit
 RT pulmonary artery smooth muscle".
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM

ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT. HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).

-1- SUBUNIT: INTEGRAL MEMBRANE PROTEIN.

-1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

-1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

-1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.

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EMBL; D45025; BAA08082.1; -

DR EMBL; AF056943; AAC13312.1; -

DR EMBL; AF149787; AAD56772.1; -

DR HSP; Q54397; 1BL8.

DR InterPro; IPR000210; BTB_P0Z.

DR InterPro; IPR001622; K-channel_pore.

DR InterPro; IPR004052; KV1channel.

DR InterPro; IPR003091; K_channel.

DR InterPro; IPR003131; K_tetra.

DR InterPro; IPR003968; Kv_channel.

DR InterPro; IPR000636; M-channel_19.

DR InterPro; IPR003972; Shaker_channel.

DR Pfam; PF00520; 1on_trans_1.

DR Pfam; PF02214; K_tetra_1.

DR PRINTS; PR00169; KCHANNEL.

DR PRINTS; PR01512; KV1CHANNEL.

DR PRINTS; PR01491; KVCHANNEL.

DR PRINTS; PR01496; SHAKERCHANNEL.

DR SMART; SM00225; BTB; 1.

KV Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Multigene family; Phosphorylation.

FT TRANSMEM 235

FT TRANSMEM 253

FT TRANSMEM 310

FT TRANSMEM 330

FT TRANSMEM 341

FT TRANSMEM 362

FT TRANSMEM 383

FT TRANSMEM 404

FT TRANSMEM 419

FT TRANSMEM 440

FT TRANSMEM 480

FT TRANSMEM 501

FT DOMAIN 78

FT DOMAIN 83

FT DOMAIN 367

FT DOMAIN 372

FT CARBOHYD 109

FT CARBOHYD 174

FT CARBOHYD 174

SO SEQUENCE 598 AA; 65475 MW; B06D235AC7A8E1F0 CRC64;

Query Match 6.28; Score 110; DB 1; Length 598;

Best Local Similarity 25.68; Pred. No. 1.1;

Matches 57; Conservative 25; Mismatches 81; Indels 60; Gaps 12;

DB 37 GCGAASASSGRRSGO---AAGR---ERAGVE-CATATLPAHCHSPSGGAAAGRMGA 89

DB 25 GCGAAPTGLGDSGSEPARGRCASAKRAEPEERPLP---QPP----- 67

QY 90 AARRAGVVVYTGREDPSRRDGMASSSDAEDD---ELEPATPYATAGHALPLLPQEPF 145

DB 68 -----ELPQGR---SPLEEEEGGDDPELSVAEQTLAGALHH----- 103

QY 146 EYVPLNIGCAHFTYRSLTACRYEDTMLAMFSG-RHYIPDSEGRYFLDRGCTHGDVYN 204

DB 104 QAVLINISGRFETOLGTLAOFPTLLGDPAKRLRYFDPLNNE--YFEDRRNPSPDGILY 161

QY 205 FLRSGD---LPPERVRAYKKAQYVAIGPLLEOLENMPK 244

DB 162 YVSGGRLRRPYNVSLDVADEIRFYQLD--EAMERFREDEG 202

RESULT 11

CIR3_RAT

ID CIR3_RAT STANDARD; PRT; 525 AA.

AC P15384.

DT 01-APR-1990 (Rel. 14, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Voltage-gated potassium channel protein Kv1.3 (RGK5) (RCK3) (KV3).

GN KCNA3.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

[1]

SEQUENCE FROM N.A.

RP TISSUE-Brain;

RC MEDLINE-90059914; PubMed-2555158;

RX Stuehmer W., Ruppersberg J.P., Schroeter K.H., Sakmann B., Stocker M., Glese K.P., Perschke A., Baumann A., Pongs O.; "Molecular basis of functional diversity of voltage-gated potassium channels in mammalian brain.";

RT EMBO J. 8:3235-3244(1989).

RL [2]

SEQUENCE FROM N.A.

RP TISSUE-Brain;

RC MEDLINE-90297965; PubMed-2361015;

RX Swanson R., Marshall J., Smith J., Williams J., Boyle M.B., Folander K., Lunau C.J., Antanavage J., Olyra C., Bunrov S.A., Bennett C., Stein R.B., Kaczmarek L.M.; "Cloning and expression of cDNA and genomic clones encoding three delayed rectifier potassium channels in rat brain.";

RT Neuron 4:929-939(1990).

RL [3]

SEQUENCE FROM N.A.

RP TISSUE-Lymphocytes;

RC MEDLINE-90278098; PubMed-2351830;

RX Douglas J., Osborne P.B., Cai Y.C., Wilkinson M., Christie M.J., Adelman J.P.; "Characterization and functional expression of a rat genomic DNA clone encoding a lymphocyte potassium channel.";

RT J. Immunol. 144:4841-4850(1990).

RL -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.

-1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

-1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

-1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.

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RN [1] SEQUENCE FROM N.A. (ALPHA ISOFORM).
 RX MEDLINE-87292096; PubMed-2441471;
 RA Tempel B.L., Papazian D.M., Schwarz T.L., Jan Y.N., Jan L.Y.,
 RT "Sequence of a probable potassium channel component encoded at Shaker
 RL locus of *Drosophila*."
 RN Science 237:770-775(1987).
 RN [2]
 RP SEQUENCE OF 1-257 FROM N.A. (BETA ISOFORM).
 RX MEDLINE-87273502; PubMed-2440582;
 RA Kamh A., Iverson L.E., Tanouye M.A.,
 RT "Molecular characterization of Shaker, a *Drosophila* gene that encodes
 RL a potassium channel."
 RN Cell 50:405-413(1987).
 RN [3]
 RP SEQUENCE FROM N.A. (DELTA ISOFORM).
 RA STRAIN-Canton-S, and Oregon-R;
 RC Baumann A., Krah-Jentgens I., Mueller R., Mueller-Holtkamp F.,
 RX Seidel R., Kecskenethy N., Casal J., Ferrus A., Pongs O.,
 RT "Molecular organization of the maternal effect region of the Shaker
 RL complex of *Drosophila*: characterization of an (I/A) channel transcript
 RN with homology to vertebrate Na(+) channel.";
 RN EMBO J. 6:3419-3429(1987).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA; GAMMA AND EPSILON).
 RC STRAIN-Canton-S;
 RX MEDLINE-88296413; PubMed-2456921;
 RA Pongs O., Kecskenethy N., Mueller R., Krah-Jentgens I.,
 RT Baumann A., Kitz H.H., Canal I., Llanazares S., Ferrus A.,
 RL "Shaker encodes a family of putative potassium channel proteins in
 RN the nervous system of *Drosophila*."
 RN EMBO J. 7:1087-1096(1988).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA; GAMMA AND B).
 RX MEDLINE-88122563; PubMed-2448633;
 RA Schwarz T.L., Tempel B.L., Papazian D.M., Jan Y.N., Jan L.Y.,
 RT "Multiple potassium-channel components are produced by alternative
 RL splicing at the Shaker locus in *Drosophila*."
 RN Nature 331:137-142(1988).
 RN [6]
 RP ERRATUM.
 RA Schwarz T.L., Tempel B.L., Papazian D.M., Jan Y.N., Jan L.Y.,
 RL Nature 332:740-740(1988).
 RN [7]
 RP SEQUENCE OF 450-534 FROM N.A.
 RC STRAIN-H4;
 RX MEDLINE-90166523; PubMed-3272175;
 RA Kamh A., Tseng-Crank J., Tanouye M.A.,
 RT "Multiple products of the *Drosophila* Shaker gene may contribute to
 RL potassium channel diversity."
 RN Neuron 1:421-430(1988).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkely;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RL Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RL Sutton G.G., Wotman J.R., Yandell M.D., Zhang Q., Chen L.Y.,
 RA Brandon R.C., Rogers J.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RL Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Adair J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandal D., Bolshakov S.,
 RA Borkova K., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pallos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Geibart W.M., Glasser K.,
 RA Glodet A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 ON NCBI_TaxID:9606;
 RN [1]
 RP MEDLINE-66149381; PubMed-2869488;
 RA Stanton L.W., Schwab M., Bishop J.M.;
 RT "Nucleotide sequence of the human N-myc gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1772-1776(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86092232; PubMed-3510398;
 RA Kohl N.E., Legouy E., Delphin R.A., Nisen P.D., Smith R.K.,
 RA Gee C.E., Alt F.W.;
 RT "Human N-myc is closely related in organization and nucleotide
 RT sequence to c-myc."
 RL Nature 319:73-77(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88202932; PubMed-2834684;
 RA Ison J.M., Rabbits P.H.;
 RT "Sequence of a germ-line N-myc gene and amplification as a mechanism
 RT of activation."
 RL Oncogene 2:399-402(1985).
 RN [4]
 RP SEQUENCE OF 71-464 FROM N.A.
 RX MEDLINE-86179901; PubMed-3008339;
 RA Slamon D.J., Boone T.C., Seeger R.C., Keith D.E., Chazin V., Lee H.C.,
 RA Souza L.M.;
 RT "Identification and characterization of the protein encoded by the
 RT human N-myc oncogene."
 RL Science 232:768-772(1986).
 RN [5]
 RP SEQUENCE OF 313-464 FROM N.A.
 RX MEDLINE-85215633; PubMed-2987858;
 RA Nischelsch R.W., Melera P.W.;
 RT "Nucleotide sequence of the 3' exon of the human N-myc gene."
 RL Nucleic Acids Res. 13:2545-2558(1985).
 RN [6]
 RP PHOSPHORYLATION BY CK2.
 RX MEDLINE-93049352; PubMed-1425701;
 RA Hagihara T., Nakaya K., Nakamura Y., Nakajima H., Nishimura S.,
 RA Taya Y.;
 RT "Specific phosphorylation of the acidic central region of the N-myc
 RT protein by casein kinase II."
 RL Eur. J. Biochem. 209:945-950(1992).
 CC -1- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR.
 CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
 CC BHLH PROTEIN. BINDS DNA AS AN HETERODIMER WITH MAX.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING FETAL DEVELOPMENT.
 CC -1- DISEASE: AMPLIFICATION OF THE N-MYC GENE IS ASSOCIATED WITH A
 CC VARIETY OF HUMAN TUMORS, MOST FREQUENTLY NEUROBLASTOMA, WHERE THE
 CC LEVEL OF AMPLIFICATION APPEARS TO INCREASE AS THE TUMOR
 CC PROGRESSES.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
 CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/genes/NMYC112.html".
 CC
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 CC
 CC EMBL: X03394; CAA27037.1; -
 CC EMBL: X03395; CAA27038.1; -
 CC EMBL: M13241; AAA36371.1; ALT_INIT.
 CC EMBL: M13228; AAA36370.1; -

DR EMBL: X02363; -. NOT_ANNOTATED_CDS.
 DR EMBL: Y00664; CAA68678.1; ALT_INIT.
 DR PIR: A25744; TVHDM2.
 DR PIR: A01355; TVHDMC.
 DR PIR: A22937; A22937.
 DR PIR: S02249; S02249.
 DR HSSP: P25912; 1HLO.
 DR TRANSFAC: T02379; -.
 DR Genew; HGNC:7559; MYCN.
 DR MIM: 164840; -.
 DR InterPro: IPR001092; HLH basic.
 DR InterPro: IPR002418; TF_MYC.
 DR Pfam: PF01010; HLH_1.
 DR Pfam: PF01056; MYC_N-term; 1.
 DR PRINTS: PR00044; LEUZIPRMYC.
 DR SMART: SM00353; HLH_1.
 DR PROSITE: PS00038; HLH_1; 1.
 DR PROSITE: PS50888; HLH_2; 1.
 KW Nuclear protein; DNA-binding; Proto-oncogene; Phosphorylation.
 FT DOMAIN 262 278
 FT DNA_BIND 381 394
 FT DOMAIN 395 434
 FT DOMAIN 433 454
 FT MOD_RES 261 261
 FT MOD_RES 263 263
 FT MOD_RES 227 227
 FT CONFLICT 363 363
 FT CONFLICT 363 363
 SQ SEQUENCE 464 AA; 49561 MW; 560E885602E30DAD CRC64;

Query Match 5.98; Score 105.5; DB 1; Length 464;
 Best Local Similarity 19.48; Pred. No. 1.7;
 Matches 71; Conservative 43; Mismatches 125; Indels 127; Gaps 14;

QY 11 GKGPLRRRLPLAL-----PALRLGELPANOG-----GTSASASS 45
 Db 100 GGLGGLTPNPVITLDDCMGFSANKEKLERAVSEKQHRGPPTAGSTASPGASAPRG 159
 QY 46 GRNSGAPAGHERVGVGATALLPPAHCLSP-----PSGAPAG-RV 85
 Db 160 RGHGGAAGAGGAGGALPAPALHAPAECDPAVVEFPVKNKEPAPVAPAPAPAGPAPV 219
 QY 86 MPGARARA-RGMVYVTGEPDSRRDG-----ANSSSAEDFELPAPITATQ 132
 Db 220 ASGAGIAAPAPAPGAPAPRPGGRTSGGDHALSTSGEDTSDDEDEE----- 271
 QY 133 AGHALPLLPQEPFVPLNIGAHFTYRLSTLCYEDTML--AAAFSGR-----H 180
 Db 272 -----DEEEDIDVYVEKRSSSMTKAVTTITIVRPKNALGGRASSLEIKR 322
 QY 181 YIPFDSRGRTYIDRDGHFGLVNLFRSGDLPFRERVAKYKAYVIAIGPLEQLENNQ 240
 Db 323 CLPFRHOHNVAAPSP-----YVESEDAPQPKIKSEASPRDLKSVIP--PRAKSL 371
 QY 241 PLNKEK-----VRAFLGLMAYYDHERIYETIARLAVOKAKARA 281
 Db 372 PRNSDSEDSERRRNHILRORRNDLRSSFTLV---RDHVELVK-----NEAAKRV 421
 QY 282 KIKSLT 287
 Db 422 ILKRAIT 427

RESULT 14
 5E5_RAT ID 5E5_RAT STANDARD; PRT; 925 AA.
 AC 063003;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE 5E5 antigen.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.

OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Name: Tissue-Brain;
 RX MEDLINE-96015159; PubMed-8537300;
 RA Suzuki E., Kojima N., Yoshimura K., Uemura K., Ohta K., Akagawa K.;
 RT Cloning and sequence analysis of cDNA for a possible DNA-binding
 RL protein 5E5 in the nervous system.
 CC J. Biochem. 118:122-128(1995).
 CC -1- FUNCTION: MIGHT HAVE DNA-BINDING ABILITY.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURONS.
 CC -----
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 CC -----
 CC EMBL: D37934; BA07153.1; -
 CC DNA-binding; Nuclear protein; Antigen.
 KW SEQUENCE 825 AA; 86831 MW; AF667FE2FD555BDF CRC64;
 SQ
 Query Match 5.9%; Score 105.5; DB 1; Length 825;
 Best Local Similarity 22.5%; Pred. No. 3.5;
 Matches 52; Conservative 18; Mismatches 56; Indels 103; Gaps 8;
 QY 10 KGGKGLR-----RRPLPALRLGELPANOOGTSAASSS-----GRS----- 49
 DB 587 RGGGRGRGRGSGSLGSTRDASPSARNGEORRRGPPAAGAAGVSTRGRARGORT 646
 QY 50 -----GQAGAGRRY-----GVEGATLPRNHCSP----- 76
 DB 647 GEEADDLPRGRDRLPRPDSNORVERPGRHGRGALNAPDASPRHPRRWVSQ 706
 QY 77 -----SCQPAAGRVPRGA---ARRAGMYV 98
 DB 707 QQRALMGFRVGGFPPRRPVLLPLRLACAGDPGSR--PGRRRARRRGELT 764
 QY 99 VTGRRPDSRRODGMSSSDAEDFLPATPTAGALPLLPQEPVVP 149
 DB 765 PQRPPAPQEGRAESCVDAIAPDTDAS-----GEVPEGP 805
 RESULT 15
 CIR2_HUMAN STANDARD; PRT; 499 AA.
 AC P16389;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Kv1.2 (BK2) (BK5) (NGK1)
 DE (MK2) (HKIV).
 GN KCNA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID-9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RA Ramaswami M., Gautam M., Kamb A., Rudy B., Tanouye M.A.,
 RA Mathew M.K.;
 RT Human potassium channel genes: molecular cloning and functional
 RT expression.
 RL Mol. Cell. Neurosci. 1:214-223(1990).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL

CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.1ab-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: I02752; AAA36141.1; -
 CC HSP: 054397; 1BLR.
 CC GeneW: HGNC:6220; KCNA2.
 DR DR
 DR MIM: 176262; -
 DR InterPro: IPR002210; BTB_P0Z.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR004049; KV12channel.
 DR InterPro: IPR003091; K+channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR006636; M+channel_nlg.
 DR InterPro: IPR003972; Shaker_channel.
 DR Pfam: PR00520; Ion_trans. 1.
 DR Pfam: PR02214; K_tetra. 1.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR01509; KV12CHANNEL.
 DR PRINTS: PR01491; KVCHANNEL.
 DR PRINTS: PR01496; SHAKERCHANNEL.
 DR SMART: SM00225; BTB. 1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 164 182 SEGMENT S1.
 FT TRANSMEM 222 243 SEGMENT S2.
 FT TRANSMEM 255 275 SEGMENT S3.
 FT TRANSMEM 293 311 SEGMENT S4.
 FT TRANSMEM 328 347 SEGMENT S5.
 FT TRANSMEM 389 411 SEGMENT S6.
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD RES 449 449 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 SQ SEQUENCE 499 AA; 56716 MW; 4B03F1B6A826C39 CRC64;
 Query Match 5.9%; Score 105; DB 1; Length 499;
 Best Local Similarity 27.9%; Pred. No. 2.1;
 Matches 41; Conservative 23; Mismatches 63; Indels 20; Gaps 6;
 QY 124 EPATPTATOGHAL-----PLLPQEPVVPYPLNIGAAHTTRISTURCTEDTMA-AMFSG 178
 DB 7 DPADAAALPGHPQDTYDPEADHECCERVYNISGLRFTQIKTLAOPETILGPKKRM 66
 QY 179 RHYIPDSEGRYFTDGTGTHGVNLFRLSGD---LPRRERYANRYKQAYVAILPLEQ 235
 DB 67 RYFDPLANE--YFDKRNPSFDALITYQSGRLRPVNPDLIFSEETRELEBEAME 124
 QY 236 L-----ENMQPL-KGEKVRQAF 252
 DB 125 MFEDEGYIKERKPLPENEFQGVWL 151

Search completed: February 12, 2003, 11:07:56
 Job time: 19 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: February 12, 2003, 11:07:36 ; Search time 13 seconds

(Without alignments)
674.097 Million cell updates/sec

Title: US-10-086-156-24

Perfect score: 1780

Sequence: 1 MVTAVLRNRKRGKPLRRP.....NNEKSPVQLPAGVFQHEMG 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	560.5	31.5	120	US-10-024-579-5	Sequence 5, Appl1
2	314.5	17.7	106	US-10-024-579-7	Sequence 7, Appl1
3	305	17.1	56	US-09-864-761-34673	Sequence 34673, A
4	245	13.8	175	US-09-925-299-879	Sequence 879, App
5	174.5	9.8	238	US-10-024-579-16	Sequence 16, Appl
6	174.5	9.8	257	US-10-024-579-14	Sequence 14, Appl
7	174.5	9.8	264	US-10-024-579-12	Sequence 12, Appl
8	174.5	9.8	283	US-10-024-579-10	Sequence 10, Appl
9	157	8.8	378	US-09-764-864-1240	Sequence 1240, Ap
10	140.5	7.9	213	US-10-024-579-2	Sequence 2, Appl1
11	127	7.1	636	US-10-062-879-4	Sequence 4, Appl1
12	127	7.1	655	US-10-062-879-2	Sequence 2, Appl1
13	120.5	6.8	532	US-09-993-811-6	Sequence 6, Appl1
14	113.5	6.4	418	US-09-946-807-3	Sequence 3, Appl1
15	113.5	6.4	418	US-09-795-668-3	Sequence 3, Appl1
16	113.5	6.4	418	US-09-819-104A-2	Sequence 2, Appl1
17	112	6.3	2507	US-09-819-104A-2	Sequence 3, Appl1
18	111	6.2	1907	US-09-832-292-39	Sequence 39, Appl
19	109	6.1	286	US-09-737-149-39	Sequence 39, Appl

20	108	6.1	351	10	US-09-350-874-61	Sequence 61, Appl
21	105.5	5.9	254	9	US-09-738-626-6616	Sequence 6616, Ap
22	104.5	5.9	447	9	US-09-975-719-351	Sequence 351, App
23	102	5.7	275	10	US-09-737-149-10	Sequence 10, Appl
24	101.5	5.7	261	9	US-09-843-676-174	Sequence 174, App
25	101.5	5.7	261	9	US-09-438-486-174	Sequence 174, App
26	101	5.7	399	10	US-09-893-737-10	Sequence 10, Appl
27	100.5	5.6	527	9	US-09-854-133-216	Sequence 216, App
28	100.5	5.6	527	10	US-09-738-973-216	Sequence 216, App
29	100	5.6	580	10	US-09-925-301-943	Sequence 943, App
30	98.5	5.5	874	10	US-09-950-370-12	Sequence 2, Appl1
31	98.5	5.5	902	10	US-09-950-370-12	Sequence 2, Appl1
32	98	5.5	687	9	US-09-764-868-661	Sequence 661, App
33	97	5.4	456	9	US-09-989-920-175	Sequence 175, App
34	97	5.4	456	10	US-09-993-811-2	Sequence 2, Appl1
35	97	5.4	456	10	US-09-974-712-2	Sequence 12, Appl
36	96.5	5.4	454	10	US-09-993-811-12	Sequence 434, App
37	96.5	5.4	1702	9	US-08-854-133-434	Sequence 434, App
38	96.5	5.4	1702	10	US-09-738-973-434	Sequence 434, App
39	94.5	5.3	7968	9	US-10-077-130-5	Sequence 5, Appl1
40	93.5	5.3	332	9	US-09-764-868-1013	Sequence 1013, App
41	93	5.2	566	9	US-09-797-500-2	Sequence 2, Appl1
42	92.5	5.2	365	9	US-10-108-605-343	Sequence 343, App
43	92.5	5.2	739	9	US-08-974-298-159	Sequence 159, App
44	92.5	5.2	739	9	US-10-028-072-478	Sequence 478, App
45	92.5	5.2	739	9	US-10-121-049-478	Sequence 478, App

ALIGNMENTS

RESULT 1
US-10-024-579-5
Sequence 5, Application US/10024579
Patent No. US20020119522A1
GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Gerhardt, Brenda
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020119522A1 Human Ion Channel-Related Proteins
FILE REFERENCE: LEX-0274-USA
CURRENT APPLICATION NUMBER: US/10/024, 579
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/258, 595
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 120
TYPE: PRT
ORGANISM: homo sapiens
US-10-024-579-5

Query Match 31.5%; Score 560.5; DB 12; Length 120;
Best Local Similarity 91.7%; Pred. No. 3.5e-40;
Matches 110; Conservative 3; Mismatches 2; Indels 5; Gaps 2;

DB 156 MVTAVLRNRKRGKPLRRP.....NNEKSPVQLPAGVFQHEMG 343
61 HETRLSLRKYEDTLMAMSGRRYIPTDSEGRYFIDRDGTHFGVSPSTINFLVLAAD 120

RESULT 2
US-10-024-579-7
Sequence 7, Application US/10024579
Patent No. US20020119522A1
GENERAL INFORMATION:

APPLICANT: Friddie, Carl Johan
APPLICANT: Gerhardt, Brenda
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020119522a1el Human Ion Channel-Related Proteins
TITLE OF INVENTION: and Polynucleotides Encoding the Same
FILE REFERENCE: Lex-0274-USA
CURRENT APPLICATION NUMBER: US/10/024,579
CURRENT FILING DATE: 2001-12-18
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 106
TYPE: PRT
ORGANISM: homo sapiens
US-10-024-579-7

Query Match 17.7%; Score 314.5; DB 12; Length 106;
Best Local Similarity 83.6%; Pred. No. 1.2e-19;
Matches 61; Conservative 5; Mismatches 2; Indels 5; Gaps 2;

QY 143 EFPEVPLNIGAHFTTSLTLCYEDTMTLAMEGRRHYIPDSEGRYIDDDGTHFCDV 202
DB 34 QFPEVPLNIGAHFTTSLTLCYEDTMTLAMEGRRHYIPDSEGRYIDDDGTHFCDV 93

QY 203 ---LNF-LNSGD 210
DB 94 SPSTINFTVVLACD 106

RESULT 3
US-09-864-761-34673
Sequence 34673, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Neomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 34673
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006001.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL - 4.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL - 12
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL - 5.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL - 4.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 7.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL - 14
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL - 8.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL - 5.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL - 2.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL - 6.4
OTHER INFORMATION: EST_HUMAN HIT: A1674184.1, EVALUE 4.00e-28
OTHER INFORMATION: SWISSPROT HIT: Q13829, EVALUE 9.00e-07
US-09-864-761-34673

Query Match 17.1%; Score 305; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.3e-19;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 EFPEVPLNIGAHFTTSLTLCYEDTMTLAMEGRRHYIPDSEGRYIDDDGTHF 199
DB 1 EFPEVPLNIGAHFTTSLTLCYEDTMTLAMEGRRHYIPDSEGRYIDDDGTHF 56

RESULT 4
US-09-925-299-879
Sequence 879, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 879
LENGTH: 175
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (168)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-879

Query Match 13.8%; Score 245; DB 10; Length 175;
Best Local Similarity 37.5%; Pred. No. 1.6e-13;
Matches 63; Conservative 26; Mismatches 63; Indels 16; Gaps 3;

QY 108 ROGAMSSDAEDDFLEPATPTAQAHALPLQLQEFPEVPLNIGAHFTTSLTLCY 167
DB 12 RPYGRMTSQTPPLPSPRRPRTMS-----TVELNNGGEPHTTGTLLRKE 57

```

Oy 168 EDMLAAEFSRHHYIPTDSEGRHYFDRCGTFHGVTLNFRSGDLPERRRVAAYKEAQY 227
      |||||
      ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|
Db 58 PGSLAAEFSSLAARASTDAESRFFIDRSTYFRPLDYLKGVY-PTQIHVEYTRAOFY 116
      |||||
      ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

Oy 228 AIGPLEOLENNMOPKGEKV-ROAFGLGIMPYKDLERIVEIARLAV 274
      |||||
      ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|
Db 117 EIKPLVTKLEDMQPIFGEGVSRKQFLLCGRATFARWMLVLAAREAI 164
      |||||
      ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

RESULT 5
; US-10-024-579-16
; Sequence 16, Application US/10024579
; Patent No. US20020119522A1
; GENERAL INFORMATION:
; APPLICANT: Fridgde, Carl Johan
; APPLICANT: Gerhardt, Brenda
; APPLICANT: Hilbun, Erin
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020119522A1el Human Ion Channel-Related Proteins
; TITLE OF INVENTION: and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0274-USA
; CURRENT APPLICATION NUMBER: US/10/024,579
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/258,595
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 238
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-024-579-16

Query Match 9.8%; Score 174.5; DB 12; Length 238;
Best Local Similarity 35.2%; Pred. No. 1.9e-07;
Matches 45; Conservative 28; Mismatches 50; Indels 5; Gaps 3;

Oy 125 PATPATQAGNATPLLPDEFPEVYVPLNTGSAFTTRLTSTICXEEDTMLAAMSGRHHYPT 184
      |||||
      ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|
Db 10 PVSPLAAQ-GIDPLPQLTRKSNAPVHIDVGHHYTSLSLATNTYTPDSKRSRLNGTEPYVL 68
      |||||
      ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

Oy 185 DS-EGRVEYIDRDGTFHGVTLNFRSGDLPERRRVA---AVYKEAQYVAIGPLEOLENNM 240
      |||||
      ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|
Db 69 DSLKMGHYFIDRNGEYFRVYLSPLFRSKILLDDPDFDFSLTYEANYQLQPVYRELERNQ 128
      |||||
      ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

Oy 241 PLKGEKVR 248
      |||||
      ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|
Db 129 QEOEQRRR 136
      |||||
      ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

RESULT 6
; US-10-024-579-14
; Sequence 14, Application US/10024579
; Patent No. US20020119522A1
; GENERAL INFORMATION:
; APPLICANT: Fridgde, Carl Johan
; APPLICANT: Gerhardt, Brenda
; APPLICANT: Hilbun, Erin
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020119522A1el Human Ion Channel-Related Proteins
; TITLE OF INVENTION: and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0274-USA
; CURRENT APPLICATION NUMBER: US/10/024,579
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/258,595
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 257
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-024-579-14

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Query Match	9.8%; Score 174.5; DB 12; Length 257;	
Best Local Similarity 35.2%; Pred. No. 2.1e-07;		
Matches 45; Conservative 28; Mismatches 50; Indels 5; Gaps 3;		
QY 125 PATPATQAGNALPLLPQEFPEVYPLNIGANFTTRSLTRCYEDPTMAAFSGRHYYPT	184	
DB 10 PVSPLAAQ-GIPLPQOLTKRSNAPVHIDVGHNYSLSLATLTKYPPSRISRLNGTEPYVL	68	
QY 185 DS-EGRYIFIDRDGTFHFQVLFNFRSGDLPERRRVR--AVYEAQYVAIGPLLEQLENNQ	240	
DB 69 DSLKHYHIDRDGEIFRYYLSLSTRISKLLLPDDEFDSLIYEANYTOLQPVRELERMQ	128	
QY 241 PLKGEKVR 248		
DB 129 QOEQRRR 136		
RESULT 7		
US-10-024-579-12		
; Sequence 12, Application US/10024579		
; Patent No. US20020119522A1		
GENERAL INFORMATION:		
APPLICANT: Friddele, Carl Johan		
APPLICANT: Gerhardt, Brenda		
APPLICANT: Hilbun, Erin		
APPLICANT: Turner, C. Alexander Jr.		
TITLE OF INVENTION: No. US20020119522A1el Human Ion Channel-Related		Proteins
TITLE OF INVENTION: and Polynucleotides Encoding the Same		
FILE REFERENCE: LEX-0274-USA		
CURRENT APPLICATION NUMBER: US/10/024, 579		
CURRENT FILING DATE: 2001-12-18		
PRIOR APPLICATION NUMBER: US 60/258,595		
PRIOR FILING DATE: 2000-12-28		
NUMBER OF SEQ ID NOS: 17		
SOFTWARE: FastSeq for Windows Version 4.0		
SEQ ID NO 12		
LENGTH: 264		
TYPE: PRT		
ORGANISM: homo sapiens		
US-10-024-579-12		
Query Match	9.8%; Score 174.5; DB 12; Length 264;	
Best Local Similarity 35.2%; Pred. No. 2.2e-07;		
Matches 45; Conservative 28; Mismatches 50; Indels 5; Gaps 3;		
QY 125 PATPATQAGNALPLLPQEFPEVYPLNIGANFTTRSLTRCYEDPTMAAFSGRHYYPT	184	
DB 36 PVSPLAAQ-GIPLPQOLTKRSNAPVHIDVGHNYSLSLATLTKYPPSRISRLNGTEPYVL	94	
QY 185 DS-EGRYIFIDRDGTFHFQVLFNFRSGDLPERRRVR--AVYEAQYVAIGPLLEQLENNQ	240	
DB 95 DSLKHYHIDRDGEIFRYYLSLSTRISKLLLPDDEFDSLIYEANYTOLQPVRELERMQ	154	
QY 241 PLKGEKVR 248		
DB 155 QOEQRRR 162		
RESULT 8		
US-10-024-579-10		
; Sequence 10, Application US/10024579		
; Patent No. US20020119522A1		
GENERAL INFORMATION:		
APPLICANT: Friddele, Carl Johan		
APPLICANT: Gerhardt, Brenda		
APPLICANT: Hilbun, Erin		
APPLICANT: Turner, C. Alexander Jr.		
TITLE OF INVENTION: No. US20020119522A1el Human Ion Channel-Related		Proteins
TITLE OF INVENTION: and Polynucleotides Encoding the Same		
FILE REFERENCE: LEX-0274-USA		
CURRENT APPLICATION NUMBER: US/10/024, 579		

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: CURRENT FILING DATE: 2001-12-18
: PRIOR APPLICATION NUMBER: US 60/258,595
: PRIOR FILING DATE: 2000-12-28
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10
: LENGTH: 283
: TYPE: PRT
: ORGANISM: homo sapiens
US-10-024-579-10

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Query Match	9.8%	Score 174.5	DB 12	Length 283
Best Local Similarity	35.2%	Pred. No. 2.4e-07		
Matches 45	Conservative 28	Mismatches 50	Indels 5	Gaps 3

```

OY 125 PATPATAOAGATALLLEPOEEFEVYVPLNIGANGHEFTPLSTISRCYDIIAMAFSESRH1PT 184
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 36 PVSPLAAQ-GIPLPAQLTKSNAPVHIDVGGHMYTSLATILTKYPDSIRISLFNGTEPIVL 94

OY 185 DS-EGREFTINDGHNFDQDYNLELSSGLPRENR---AYKKQOXYAAIGLPIGLELNMQ 240
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 95 DSLKOHFTINDGGEFTRYVLSFTLSKLLPDPDKDSLLEENKRYIQLQAGVAVNEEDRMQ 150
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```
QY      241 PLKGEKVR 248
Db      155 QEQEQRRR 162
```

RESULT 9
US-09-764-864-1240

```

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT723
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1240

```

```

?      :      :      :      :      :      :      :      :      :      :      :      :
?      : ORGANISM: Homo sapiens
?      : FEATURE:
?      : NAME/KEY: SITE
?      : LOCATION: (51)
?      : OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
?      : NAME/KEY: SITE
?      : LOCATION: (76)
?      : OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
?      : NAME/KEY: SITE
?      : LOCATION: (358)
?      : OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1240

Query Match          8.8%; Score 157; DB 10; Length 378;
Best Local Similarity 29.4%; Pred. No. 1e-05;
Matches    68; Conservative 29; Mismatches 76; Indels 56; Gaps 12
```

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Oy 106 --SRROGAMSSS-----DAEDD-----FLPAPTPYAOGHAPL 139
      : : | :: | | | | :
.db 47 LSVASRKGIRKATSVYNGKGLDIDIALIXDDVLFVCECEPFIPOQTDNRPEG----- 101

```

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QY      140 LEQEFPEVPLNIGAGHFTTRISTLRCE-DTMLAMF--SGRHYPIDSEGRYFLDRDG 196
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      102 LIGFHTDMLTLNAGRYFTTTRSTLVNKEPDSMLAHMFKDKGCVWGNKQDHGAFLLDRSP 161

```

```

QY      197 THEGVLNPLRSGDLPFRKVR--AVYKEAYYAIGPLLEQL-----NMQP 2411
      :| :||:| | | : : | :||:| | | :| | |
DB      162 EYFEPILNYLRHGQLIVNDGINLGLVLEAFEGIDSLIEHLEVAIKNSQP 2122

```

RESULT 10
US-10-024-579-2
; Sequence 2, Application US/10024579
; Patent No. US20020119522A1
; Summary Information

. APPLICANT: Fiddle, Carl Johan
 . APPLICANT: Gerhardt, Brenda
 . APPLICANT: Hilbun, Erin
 . APPLICANT: Turner, C. Alexander Jr.
 . TITLE OF INVENTION: No. US20020119522a1el Human Ion Channel-Related Proteins
 . TITLE OF INVENTION: and Polynucleotides Encoding the Same
 . FILE REFERENCE: LEX-0274-USA
 . CURRENT APPLICATION NUMBER: US/10/024,579
 . CURRENT FILING DATE: 2001-12-18
 . PRIOR APPLICATION NUMBER: US 60/258,595
 . PRIOR FILING DATE: 2000-12-28

```

; SEQ ID NO 2
; LENGTH: 213
; TYPE: prt
; ORGANISM: homo sapiens
US-10-024-579-2

```

[illegible]

```

RESULT 11
US-10-062-879-4
; Sequence 4, Application US/10062879
; Patent No. US20020127649A1
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Diks, Daniel W.
; APPLICANT: Chang Ling, Hui-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; TITLE OF INVENTION: Polypeptides and Uses Therefor
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/10/062,379
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178,103
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 636
; TYPE: prt
; ORGANISM: human
US-10-062-879-4

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Query Match: 7 18; Score 127; DB: 12; Length 636;
 Best Local Similarity 34.78; Pred. No. 0.0065;
 Matches 35; Conservative 15; Mismatches 43; Indels 8; Gaps 3;

```

QY 137 LPLP---QEEVVPINIGAHFTTRTSTLCRYEDTMLAMFSGRHYIPDSEGRYFI 19
      :| | : | : | | | | | | | : : : : | |
Db 27 MPLAPADKNKRODELIYVNSGRGFQTRWTRTLERFPTLBS--TEKEFFFNEDTKETFF 84

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Wed Feb 12 12:05:08 2003

us-10-086-156-24.rabb

Page 6

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 418
; TYPE: prt
; ORGANISM: Homo sapiens
DS-09-795-668-3

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Query Match	6.4%;	Score 113.5;	DB 10;	length 418;
Best Local Similarity	24.5%;	Pred. No. 0.051;		
Matches	73;	Conservative	31;	Mismatches 93;
			Indels	101;
			Gaps	15;

```

OY 9 RKKGCGRRRRPL-----LPLRTGCELPANOGGSAASAGRRSGAPGRRXGV 61
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 9 RSGRRGRRAGRRSAASSPLPLPLLLL-----GRAGGAAAGNNA--APAG----- 56
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 62 EGATLPPAHCLSPSPGQAPAGRVPGANBARANOVVVTGRRPDSRRQDGAMS----- 114
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 57 -----ASVCSPPS-----VGSVOELAGRAA--VYIECKVHPORQOGALTRKAAAA 101
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 115 -----SSDDEDDFLE-----PATPAT-----QAGHALPLPQEF 144
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 102 GCAAGAGGDRPPAAGRRALGPRAEPELLANGTVBWPAPAPPSAGPEBEAPYL-VKV 160
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 145 PEVVPPLNIG---AHFTTLSTLRCYEDTLAMFSGRRYIPT-----DSGRYFIDR 194
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 161 HQVAVYKAGGKXKNDLLTVRGTV-----GHAFPSGCRKLEDSRIYFMEP 207
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 195 DQTHRGDVLNLRSGDLPREPRVAVYKE-----AQYVYAGLLEOLEENNOPLKGEV 247
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 208 DANSTRAPALFRA-SFFPLETGRLNKKVEYSRYLCKKCALPRLKKEKSSQSAAGSKL 264
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

```
Search completed: February 12, 2003, 11:09:42
Job time : 15 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:07:30 ; Search time 21 Seconds

(without alignments)
1570.196 Million cell updates/sec

Title: US-10-086-156-24

Sequence: 1 MFMVLRNRKRGKGLRRRP.....NNEKSPVQLPAGVFOHFG 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database : PIR 73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	200	11.2	220	2 T20366	hypothetical prote
2	175	9.8	348	2 A41784	tumor necrosis fac
3	160.5	9.0	134	2 T23065	hypothetical prote
4	146.5	8.2	651	2 A39372	potassium channel
5	144.5	8.1	212	2 T31997	hypothetical prote
6	143.5	8.1	373	2 T26885	hypothetical prote
7	143	8.0	190	2 T26019	hypothetical prote
8	137.5	7.7	204	2 T25972	hypothetical prote
9	134	7.5	208	2 T25973	hypothetical prote
10	134	7.5	231	2 T32070	hypothetical prote
11	133.5	7.4	140	2 T25976	hypothetical prote
12	132	7.4	179	2 T33590	hypothetical prote
13	132	7.4	670	2 T33221	hypothetical prote
14	131.5	7.4	246	2 T25978	hypothetical prote
15	131	7.4	220	2 T33592	hypothetical prote
16	131	7.4	244	2 T25970	hypothetical prote
17	130.5	7.3	261	2 T24532	hypothetical prote
18	127	7.1	236	2 T33589	hypothetical prote
19	124.5	7.0	272	2 T15820	hypothetical prote
20	123	6.9	207	2 T31996	hypothetical prote
21	123	6.9	460	2 S11558	transforming prote
22	123	6.9	460	2 T27759	hypothetical prote
23	121.5	6.8	326	2 T32067	hypothetical prote
24	121	6.8	490	2 A35312	potassium channel
25	121	6.8	514	2 C49507	potassium channel
26	121	6.8	602	2 A49507	potassium channel
27	121	6.8	630	2 T30271	voltage-sensitive
28	118	6.6	139	2 T32068	hypothetical prote
29	117.5	6.6	135	2 T25980	hypothetical prote

30	117.5	6.6	155	2 T25979	hypothetical prote
31	116.5	6.5	285	2 T25971	hypothetical prote
32	115	6.5	441	2 C85362	hypothetical prote
33	115	6.5	597	2 S51212	BAK5 protein - boy
34	114	6.4	1791	2 T02345	hypothetical prote
35	113.5	6.4	139	2 T25974	hypothetical prote
36	113.5	6.4	265	2 T32015	hypothetical prote
37	113.5	6.4	602	2 T30166	hypothetical prote
38	113.5	6.4	613	2 A56031	potassium voltage-
39	112	6.3	1495	2 S60255	transcription co-r
40	111.5	6.3	643	2 S00480	potassium channel
41	110.5	6.2	84	2 T25977	hypothetical prote
42	110	6.2	227	2 T33591	hypothetical prote
43	110	6.2	598	2 S6669	potassium channel
44	109	6.1	441	2 C84634	hypothetical prote
45	108.5	6.1	422	2 S32357	glial growth facto

ALIGNMENTS

RESULT 1
T20366
hypothetical protein D2045.8 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T20366
R/Lloyd, C.
submitted to the EMBL Data Library, August 1994
A/Reference number: Z19262
A/Accession: T20366
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-220 <WIL>
A/Cross-references: EMBL:Z35639; PIDN:CA84696.1; GSDDB:GN00021; CESP:D2045.8
A/Experimental source: clone D2045
C/Genetics:
A/Map position: 3
A/Map position: 3
A/Introns: 39/3; 127/3; 169/1; 194/3

Query Match 11.2% Score 200; DB 2; Length 220;
Best Local Similarity 35.6% Pred. No. 1.1e-07;
Matches 64; Conservative 22; Mismatches 46; Indels 48; Gaps 10;

OY 123 LEPAPEPTAQAGALPLPQEPPEVPLNIGAHFTRLSTLCYEDTMLAAMSGRHXY 182
Db 1 MEPSI-----IVKLDVGKIKFTTFTL-CKHDSMTKMTCTDVPV 40

OY 183 PTDSGRYFIDRDGTHFGDVLNPLRSGD--LPPRR-VRAVYKDAQYAIQPLEOLENM 239
Db 41 TRNEGSVFIDSDSKHFRILNPLRSGDQALPDSDEVRYLAASFLDPLIE----- 95

OY 240 QPLKEKYRQAFGLMPYKDKLERIVEIAFLRAVQRKARFALKSLTPSMLMSVLTIMP 299
Db 96 --LGERLEQS---LNPYR--HLVSTV-----LEA--RKIFATKEKP-----VVLRLP 135

RESULT 2
A41784
tumor necrosis factor-alpha-induced protein B12 - human
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 29-Aug-1997
C/Accession: A41784
R/Wolf, F.W.; Marks, R.M.; Sarmé, V.; Byers, M.G.; Katz, R.W.; Shows, T.B.; Dixit, V.
J. Biol. Chem. 267, 1317-1326, 1992
A/Title: Characterization of a novel tumor necrosis factor-alpha-induced endothelial
A/Reference number: A41784; MUID:92112779; PMID:1370465
A/Accession: A41784
A/Molecule type: mRNA
A/Residues: 1-348 <WOL>
A/Note: sequence extracted from NCBI backbone (NCBIN:76547, NCBI:76550)
A/Note: It is uncertain whether Met-1 or Met-33 is the initiator

1
2
3
4
5

A;ResIdues: 1-373 <WIL>

A:Cross-references: EMBL:AL032639; PIDN:CAA21638.1; GSPDB:GN00020; CESP:F18A11.5
 A:Experimental source: clone Y38F1A
 C:Genetics:
 A:Gene: CESP:F18A11.5
 A:Map position: 2
 A:Introns: 7/3; 44/3; 99/3; 152/2; 198/3; 223/1

Query Match 8.1%; Score 143.5; DB 2; Length 373;
 Best Local Similarity 43.2%; Pred. No. 0.0033;
 Matches 41; Conservative 12; Mismatches 33; Indels 9; Gaps 5;

QY 146 EYVPLNIGAHHTTSLTACEDTFLAMFSGRHYIPTDSEGRYFIDRGTHFGDVLNF 205
 DB 20 ERYLVNIGVGGKKEFTVATLTVSDVLAIVSDRW--KTGDE--IFIDRDPKHFGKVLNT 75

QY 206 LRSGL--LPP--RERYRAYKEAQAAYAGPLLEQL 236
 DB 76 LRQGHFVAPSDTEACDELKRAHRYNM--PFLAEM 109

RESULT 7

T25973

hypothetical protein VM106R.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T25973
 R:Wu, X.; Kramer, J.
 A:Submitted to the EMBL Data Library, August 1998
 A:Reference number: Z20135

A:Accession: T26019
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-190 <MW>

A:Cross-references: EMBL:AL031266; PIDN:CAA20329.1; GSPDB:GN00020; CESP:VM106R.1

A:Experimental source: clone VM106R

C:Genetics:

A:Gene: CESP:VM106R.1

A:Map position: 2

A:Introns: 131/1

Query Match 8.0%; Score 143; DB 2; Length 190;
 Best Local Similarity 36.1%; Pred. No. 0.0015;
 Matches 39; Conservative 18; Mismatches 39; Indels 12; Gaps 3;

QY 146 EYVPLNIGAHHTTSLTACEDTFLAMFSG-----RHYIPTDSEGRYFIDRGTHF 199
 DB 6 DVTIANVGSTMTTTRSTISKETDILLANIASGSLSEDEQANVTYLPDGLTFVDRDGLP 65

QY 200 GDVLFNRSGDLPPEPRVAVYK---EAQYVAI--GPLEOLENNOP 241
 DB 66 AYVLFNRDKLSLPEQPREVARLKEADFYRLERSSTILSNASTISP 113

RESULT 8

T25972

hypothetical protein ZC239.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T25972
 R:Wu, X.; Kramer, J.
 A:Submitted to the EMBL Data Library, December 1996
 A:Description: The sequence of C. elegans cosmid ZC239.
 A:Reference number: Z20117

A:Accession: T25972

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-204 <MW>

A:Cross-references: EMBL:U080442; PIDN:AAB37944.1; GSPDB:GN00020; CESP:ZC239.5

A:Experimental source: strain Bristol N2; clone ZC239

C:Genetics:

A:Gene: CESP:ZC239.5

A:Map position: 2

A:Introns: 38/3; 115/3; 135/1

Query Match 7.7%; Score 137.5; DB 2; Length 204;
 Best Local Similarity 30.5%; Pred. No. 0.0043;
 Matches 40; Conservative 21; Mismatches 47; Indels 23; Gaps 6;

QY 147 VYVPLNIGAHHTTSLTACEDTFLAMFSGRHYIPTDSEGR-----YFIDRGTHFGD 201
 DB 5 IRLNIVGKKEFTVATL-----TRFEGFKOKTRGKIQWOTTLFIDRSPTHFEI 55

QY 202 VLNFRSG--DLPPR--ERYRAYKEAQAAYAGPLLEOLEN--MGLPGEKRAQAFGLMPY 257
 DB 56 ILNFRDQKVDLPETLKEMLPIFREYTYTLASLVQCGAIALSGGPFDFKRGILP 114

QY 258 YKDLERIVEI 268
 DB 115 ----TEAVVSI 121

RESULT 9

T25973

hypothetical protein ZC239.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T25973
 R:Wu, X.; Kramer, J.
 A:Submitted to the EMBL Data Library, December 1996
 A:Description: The sequence of C. elegans cosmid ZC239.
 A:Reference number: Z20117

A:Accession: T25973
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-208 <MW>

A:Cross-references: EMBL:U080442; PIDN:AAB37941.1; GSPDB:GN00020; CESP:ZC239.4

A:Experimental source: strain Bristol N2; clone ZC239

C:Genetics:

A:Gene: CESP:ZC239.4

A:Map position: 2

A:Introns: 37/3; 133/3; 175/1

Query Match 7.5%; Score 134; DB 2; Length 208;
 Best Local Similarity 38.3%; Pred. No. 0.008;
 Matches 36; Conservative 12; Mismatches 42; Indels 4; Gaps 3;

QY 146 EYVPLNIGAHHTTSLTACEDTFLAMFSGRHYIPTDSEGRYFIDRGTHFGDVLNF 205
 DB 3 EAVKLDVGGTITKTSITLTF--DGFRTMLGSGICLNDESGCIFIDRSPKHFLLTNF 61

QY 206 LRSGL--DLPPR--RAYVKEAQAAYAGPLLEQL 236
 DB 62 MRDGLALPKNDRDLTFLMAEAQYVILLDGLIDRL 95

RESULT 10

T32070

hypothetical protein F22E5.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
 C:Accession: T32070
 R:Graves, T.; Wohldmann, P.; Clarke, K.
 A:Submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of C. elegans cosmid F22E5.
 A:Reference number: Z21119

A:Accession: T32070

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-231 <GRA>

A:Cross-references: EMBL:AF016681; PIDN:AAB66172.1; GSPDB:GN00020; CESP:F22E5.6

A:Experimental source: strain Bristol N2; clone F22E5

C:Genetics:

A:Gene: CESP:F22E5.6

A:Map position: 2

A:Introns: 40/3; 125/3; 170/1

C:Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12

Query Match 7.48; Score 134; DB 2; Length 231;

Best Local Similarity 39.48; Pred. No. 0.0092;

Matches 37; Conservative 10; Mismatches 41; Indels 6; Gaps 3;

QY 146 EVPLNIGGAFTTRLSRCEYEDTMAAMFGSRHYIPDSEGRYIDRDGTHFGVNL 205

DB 6 EKILNIGGTFETSKSLTKF-DSEFKTLETDIPIQKDSNCIFIDRSPRFEKILNT 64

QY 206 LRSG--DLPP--RRVRAVYKEAOYAIQPLLE 234

DB 65 LRSGADVDLPPESERKEKRAQFYLLEGLME 98

RESULT 11

T25976 hypothetical protein ZC239.14 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T25976

R:Wu, X.; Kramer, J.

A:Description: The sequence of C. elegans cosmid ZC239.

A:Reference number: Z20117

A:Accession: T25976

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-140 <NUC>

A:Cross-references: EMBL:U08042; PIDN:AA37956.1; GSPDB:GN00020; CESP:ZC239.14

A:Experimental source: strain Bristol N2; clone ZC239

C:Genetics:

A:Gene: CESP:ZC239.14

A:Map position: 2

A:Intons: 37/3; 132/1

Query Match 7.48; Score 132.5; DB 2; Length 140;

Best Local Similarity 34.98; Pred. No. 0.0063;

Matches 38; Conservative 19; Mismatches 41; Indels 11; Gaps 5;

QY 146 EVPLNIGGAFTTRLSRCEYEDTMAAMFGSRHYIPDSEGRYIDRDGTHFGDV 202

DB 3 EVPLNIGGAFTTRLSRCEYEDTMAAMFGSRHYIPDSEGRYIDRDGTHFGDV 58

QY 203 LNFRLSGD--LPRE--RVRAVYKEAOYAIQPLLEENM-PLGKEXV 247

DB 59 LNFRLSGD--LPRE--RVRAVYKEAOYAIQPLLEENM-PLGKEXV 107

RESULT 12

T23590 hypothetical protein C40A11.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000

C:Accession: T23590

R:Magill, T.; Goela, D.

A:Description: The sequence of C. elegans cosmid C40A11.

A:Reference number: Z21374

A:Accession: T23590

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-179 <NUC>

A:Cross-references: EMBL:AF099914; PIDN:AA66757.1; GSPDB:GN00020; CESP:C40A11.6

A:Experimental source: strain Bristol N2; clone C40A11

C:Genetics:

A:Gene: CESP:C40A11.6

A:Map position: 2

A:Intons: 40/3; 123/3

C:Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12

Query Match 7.48; Score 132; DB 2; Length 179;

Best Local Similarity 36.88; Pred. No. 0.0093;

Matches 39; Conservative 21; Mismatches 36; Indels 10; Gaps 6;

QY 147 VPLNIGGAFTTRLSRCEYEDTMAAMFGSRHYIPDSEGRYIDRDGTHFGVNL 206

DB 7 IVKLNVGSVETWKSSTL-TKODGFFKTLIENNVVKKDTSDCYTIDRSPKFEYLVNM 65

QY 207 RSG--DLPP--RVRAVYKEAOYAIQPLLEENM-PLGKEXV 248

DB 66 RSGVTVLPDSERKEKELKEAEFY--LLEHVLDPCEPK-NKIR 106

RESULT 13

T23221 hypothetical protein T23B12.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T23221

R:Davidson, S.; Wohldmann, P.; Giliam, B.

A:Description: The sequence of C. elegans cosmid T23B12.

A:Reference number: Z21137

A:Accession: T23221

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-670 <DNA>

A:Cross-references: EMBL:AF022982; PIDN:AA69932.1; GSPDB:GN00023; CESP:T23B12.6

A:Experimental source: strain Bristol N2; clone T23B12

C:Genetics:

A:Gene: CESP:T23B12.6

A:Map position: 5

A:Intons: 87/2; 185/3; 293/1; 400/1; 457/1; 540/2; 635/3

Query Match 7.48; Score 132; DB 2; Length 670;

Best Local Similarity 31.28; Pred. No. 0.05;

Matches 35; Conservative 20; Mismatches 55; Indels 2; Gaps 2;

QY 147 VPLNIGGAFTTRLSRCEYEDTMAAMFGSRHYIPDSEGRYIDRDGTHFGVNL 206

DB 20 IVNVLNIGGTFETSKSLTKF-DSEFKTLETDIPIQKDSNCIFIDRSPRFEKILNT 79

QY 207 RSGDLP--PREVRAVYKEAOYAIQPLLEENM-PLGKEXV 256

DB 80 RSGDLP--PREVRAVYKEAOYAIQPLLEENM-PLGKEXV 131

RESULT 14

T25978 hypothetical protein ZC239.15 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T25978

R:Wu, X.; Kramer, J.

A:Description: The sequence of C. elegans cosmid ZC239.

A:Reference number: Z20117

A:Accession: T25978

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-246 <NUC>

A:Cross-references: EMBL:U08042; PIDN:AA37955.1; GSPDB:GN00020; CESP:ZC239.15

A:Experimental source: strain Bristol N2; clone ZC239

C:Genetics:

A:Gene: CESP:ZC239.15

A:Map position: 2

A:Intons: 37/3; 127/3

C:Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12

Query Match 7.48; Score 131.5; DB 2; Length 246;

Best Local Similarity 30.28; Pred. No. 0.015;

Matches 42; Conservative 27; Mismatches 49; Indels 21; Gaps 6;

QY 146 EVPLNIGGAFTTRLSRCEYEDTMAAMFGSRHYIPDSEGRYIDRDGTHFGDV 202

Db 3 ETVKIDVAGTIFKTSRSLTFKNGFFKTMLESIDG----LKIDSGSIFIDNSPKNFDLI 58
 QY 203 LNFIRSGD-LPPRE-RVRAVYKEAQYVYAGPLLEOLEN-MQPLKGEKYROAFLGLMPY 258
 Db 59 LNFMRDGDVYLPNCELKKEKELVEAQFLLDGLIELCNSKIELVEAPKIKLRF----- 111
 QY 259 KDHLERIVEIARLRAVORK 277
 Db 112 --IESDEQFLOQLAVOOK 127

RESULT 15

T33592

hypothetical protein C40A11.7 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000

C/Accession: T33592

R/Magyl, L., Goela, D.

Submitted to the EMBL Data Library, October 1998

A/Description: The sequence of C. elegans cosmid C40A11.

A/Reference number: 221374

A/Accession: T33592

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-220 <MAG>

A/Cross-references: EMBL:AF099914; PIDN:MAC68762.1; GSPDB:GN00020; CESP:C40A11.7

A/Experimental source: strain Bristol N2; clone C40A11

C/Genetics:

A/Gene: CESP:C40A11.7

A/Map position: 2

A/Intons: 40/3; 123/3; 162/1

C/Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12

Query Match 7.4%; Score 131; DB 2; Length 220;

Best Local Similarity 31.1%; Pred. No. 0.014;

Matches 42; Conservative 26; Mismatches 45; Indels 22; Gaps 7;

QY 147 VVPLNIGGAHFTTRISTRTCTEDYMLAMFSGRAHYIPDSEGRYFIDRDGTHFGDVLNFI 206
 Db 7 IVKLNVGSGVFEYWKSTL-TKODGFFKTLVETNIPVKDTSQCYFIDRSRPFYEVLYNFM 65
 QY 207 RSG--DLPFRER-VRAVYKEAQYVYAGPLLEOLEN-MQPLKGEKYROAFLGLMPYTKDHL 262
 Db 66 RSGVTVPDSEKELEKKEAFY---LLEQLVDLCEPINNO-----INTYRSSH- 112
 QY 263 ERIVEIARLRAVORK 277
 Db 113 ----ELQIITASTK 123

Search completed: February 12, 2003, 11:09:01
 Job time : 23 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:06:15 / Search time 34 Seconds
(without alignments)
2078.652 Million cell updates/sec

Title: US-10-086-156-24

Perfect score: 1780

Sequence: 1 MIVAVLNRRKGGKGPLRRRP.....NNEKSPVQLPAGVQHFWMG 343

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_ricent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	981	55.1	289	4	Q96MP8
2	584	32.8	214	6	Q9BE68
3	274	15.4	225	4	Q9B013
4	245.5	13.8	290	11	Q9CU79
5	244	13.7	234	11	Q8R3T6
6	211.5	11.9	228	4	Q8RC65
7	208	11.7	315	11	Q922M3
8	206	11.6	310	4	Q96SU0
9	206	11.5	313	4	Q9H3F6
10	204	11.5	329	4	Q9GSA1
11	204	11.5	329	4	Q8WZ19
12	200	11.2	320	5	Q18986
13	186	11.0	301	5	Q9V9F4
14	193	10.8	329	4	Q96P93
15	192.5	10.8	333	4	Q8WUN2
16	189.5	10.6	338	5	Q9WZF9

17	180.5	10.1	228	5	Q9VDH3	Q9VDH3 drosophila
18	180	10.1	298	10	Q9SE95	Q9SE95 arabidopsis
19	180	10.1	707	4	Q8W993	Q8W993 homo sapien
20	180	10.1	707	4	Q8TBC3	Q8TBC3 homo sapien
21	177.5	10.0	259	11	Q9C9K4	Q9C9K4 mus sapien
22	176	9.9	704	11	Q9ES31	Q9ES31 mus sapien
23	174.5	9.8	283	4	Q96S11	Q96S11 homo sapien
24	174.5	9.8	730	5	Q9VH62	Q9VH62 drosophila
25	172	9.7	316	11	Q70479	Q70479 mus sapien
26	170.5	9.6	259	4	Q8W9F5	Q8W9F5 homo sapien
27	170.5	9.6	259	11	Q9D7X1	Q9D7X1 mus sapien
28	168.5	9.5	234	4	Q9BV16	Q9BV16 homo sapien
29	165	9.3	815	4	Q9Y5V7	Q9Y5V7 homo sapien
30	165	9.3	815	4	Q8WX16	Q8WX16 homo sapien
31	164.5	9.2	234	4	Q96N73	Q96N73 homo sapien
32	163.5	9.2	435	4	Q962M9	Q962M9 homo sapien
33	159	8.9	247	4	Q96G52	Q96G52 homo sapien
34	159	8.9	290	4	Q95517	Q95517 homo sapien
35	152.5	8.9	325	4	Q96CX2	Q96CX2 homo sapien
36	152.5	8.6	234	11	Q8VC57	Q8VC57 mus sapien
37	150.5	8.5	276	5	Q16706	Q16706 caenorhabditis
38	147	8.3	234	4	Q9XV2	Q9XV2 homo sapien
39	146.5	8.2	647	4	Q9MSA2	Q9MSA2 homo sapien
40	146.5	8.2	647	4	Q75671	Q75671 homo sapien
41	146.5	8.2	651	11	Q03719	Q03719 mus sapien
42	144.5	8.1	212	5	Q16613	Q16613 caenorhabditis
43	143.5	8.1	373	5	Q9XWL7	Q9XWL7 caenorhabditis
44	143	8.0	190	5	Q9XKA3	Q9XKA3 caenorhabditis
45	139.3	7.8	632	13	Q8WU33	Q8WU33 gallus galli

ALIGNMENTS

RESULT 1

Q96MP8 PRELIMINARY; PRT; 289 AA.

AC Q96MP8; 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 20, Last annotation update)

DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE CDNA FLJ32069 f1s, clone OCBF100018, weakly similar to tumor necrosis factor, alpha-1-induced protein 1, endothelial.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID:9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RA Osima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Mueashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagauma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuno Y., Nagai K., Isogai T., "NEBO human cDNA sequencing project"; Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; AK056631; BAB71236.1; -

DR InterPro; IPR003131; K.tetra.

DR InterPro; IPR003580; Prochakylint.

DR Pfam; PF02214; K.tetra; 1.

DR SMART; SM00203; TK; 1.

SO SEQUENCE 289 AA; 33132 MW; 1FD1F618CD5E459 CRC64;

Query Match 55.1%; Score 981; DB 4; Length 289;

Best Local Similarity 100.0%; Pred. No. 1.7e-66; Mismatches 0; Indels 0; Gaps 0;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 MIVAVTGRPDSPRQDGMSSSDAEDDFLEPAPATAGAHPLLPDPFPPVPLNTGGA 155

DB 1 MIVAVTGRPDSPRQDGMSSSDAEDDFLEPAPATAGAHPLLPDPFPPVPLNTGGA 60

OY 156 HETRLSTLRCYEDTMTAAFGSGRHYIPDSRGYFIDRGTGFGVNLNLSGDLPPRE 215
 DB 61 HETRLSTLRCYEDTMTAAFGSGRHYIPDSRGYFIDRGTGFGVNLNLSGDLPPRE 120
 OY 216 RYRAYKKAQYVAYIGPLLEQLENNQPLKGEKVRQAFGLMPYKDLERIVELARAVQ 275
 DB 121 RYRAYKKAQYVAYIGPLLEQLENNQPLKGEKVRQAFGLMPYKDLERIVELARAVQ 180
 OY 276 RYRAYKKAQ 284
 DB 181 RYRAYKKAQ 189

RESULT 2

OYB68 PRELIMINARY: PRT: 214 AA.
 AC 09B68: PRELIMINARY: PRT: 214 AA.
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Hypothetical 25.0 kDa protein.
 OS Macaca fascicularis (Crad eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FRONTAL LOBE LEFT;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terno K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries.
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB056802; BAB39326.1;
 DR InterPro: IPR003131; K_tetra.
 DR Pfam: PF02214; K_tetra; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 214 AA; 25001 MW; FBD124AB711EB5 CRC64;

Query Match 32.8%; Score 584; DB 6; Length 214;
 Best Local Similarity 99.1%; Pred. No. 1.3e-36;
 Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 171 MAAFGSGRHYIPDSRGYFIDRGTGFGVNLNLSGDLPPREYRAYKKAQYVAYIG 230
 DB 1 MAAFGSGRHYIPDSRGYFIDRGTGFGVNLNLSGDLPPREYRAYKKAQYVAYIG 60
 OY 231 PLEQLENNQPLKGEKVRQAFGLMPYKDLERIVELARAVQKARAFK 284
 DB 61 PLEQLENNQPLKGEKVRQAFGLMPYKDLERIVELARAVQKARAFK 114

RESULT 3

OYB013 PRELIMINARY: PRT: 225 AA.
 AC 09B013: PRELIMINARY: PRT: 225 AA.
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE Unknown (protein for MGC:3993) (protein for MGC:12376).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Strausberg R.;
 RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RC TISSUE=LUNG;
 RA Strausberg R.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC001929; AAH01929.1;
 DR EMBL; BC001062; AAH01062.1;
 DR InterPro: IPR000210; BTB_P02.
 DR InterPro: IPR003131; K_tetra.
 DR Pfam: PF02214; K_tetra; 1.
 DR SMART: SM00225; BTB; 1.
 SQ SEQUENCE 225 AA; 26188 MW; BA8435C5D6C2476D CRC64;

Query Match 15.4%; Score 274; DB 4; Length 225;
 Best Local Similarity 45.7%; Pred. No. 4e-13;
 Matches 59; Conservative 27; Mismatches 41; Indels 2; Gaps 2;

OY 147 VPLNIGAHFTLSTLRCYEDTMTAAFGSGRHYIPDSRGYFIDRGTGFGVNLNLSGDLPPRE 206
 DB 4 VPLNIGAHFTLSTLRCYEDTMTAAFGSGRHYIPDSRGYFIDRGTGFGVNLNLSGDLPPRE 63
 OY 207 RSGDLPPREYRAYKKAQYVAYIGPLLEQLENNQPLKGEKVRQAFGLMPYKDLERIVELARAVQ 265
 DB 64 RTGVY-PGCHIDEYVREAFYKIKPLKLEDDMPQIFGSEYVRKQPLQVPGISENLELM 122
 OY 266 VEIARAV 274
 DB 123 VEIARAV 131

RESULT 4

OYB079 PRELIMINARY: PRT: 290 AA.
 AC 09B079: PRELIMINARY: PRT: 290 AA.
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE 3430433B02Rik protein (fragment).
 GN 3430433B02Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=HEAD;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glass C., King B., Kocikova H.,
 RA Kuehl P., Lewis S., Matano Y., Nakai I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazarinelli J., Mombarts P.,
 RA Nordone P., Rung B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz K., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK017384; BAB30722.1;
 DR MGD; MGI:1918643; 5430433B02Rik.
 DR InterPro: IPR000210; BTB_P02.
 DR InterPro: IPR003131; K_tetra.
 DR Pfam: PF02214; K_tetra; 1.
 DR SMART: SM00225; BTB; 1.
 FT NON_TER 1
 SQ SEQUENCE 290 AA; 31443 MW; 1AB511251CEB005 CRC64;

Query Match 13.8%; Score 245.5; DB 11; Length 290;
 Best Local Similarity 28.7%; Pred. No. 8e-11;
 Matches 93; Conservative 37; Mismatches 103; Indels 91; Gaps 12;

QY 16 LRRRLPALPRLGLPLPANGG--TSASASGSRSGCAPAGHERVGEATLPAHCL 73
 DB 1 LRRR---RPRRAAGATPGSGSLVPSAAAAATAAAAGR-----GLRPRARAL 50
 QY 74 SPSPGQPAAGVMPGAPRARGVVTGRRPDSRRDQAMSSSDADDFLEPATPTATQA 133
 DB 51 GPPAS-----PG--RVASALVQY-----PRLSSSDAYLEQDNG-----DW 85
 QY 134 GHALPLPQEPPEVPLNIGAHFTTRSLTLCYEDTMLAAMFGSRHYIPTDEGRYFID 193
 DB 86 GYMM-----SDPYTLNAGHLTYTSLTLTRYPDSMLGAMFGDPPARADPOGNFID 138
 QY 194 RDGHFEGVNLFRSGDLP---PRERAVRYEAOYTAIGPLLEQENMOPKGEKYRQA 250
 DB 139 RDGPLEFRVYLNFTSELTLPLDFKEFDLRKADFTQIEPLQCLNDPRPL----- 190
 QY 251 FLGMPYKDHLEIRVEIARLAVORRKA-----FAKLKSL----- 286
 DB 191 -----YMDFFEEVVELSSTRKLSKSNPVAIITQTLTTTVSHLSGISNYFTKMK 244
 QY 287 -----PSPWLSVLIKMPGYTS 304
 DB 245 HMMPEFASLHMTVTRIPGSLIS 268

RESULT 5

Q8R3T6 PRELIMINARY; PRT; 234 AA.

AC 08R3T6;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DE Similar to hypothetical protein MGC2376.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC024588; AAH24588.1;
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 27008 MW; F727A35094F516FA CRC64;

Query Match 13.7%; Score 244; DB 11; Length 234;
 Best Local Similarity 41.2%; Pred. No. 7.9e-11;
 Matches 56; Conservative 34; Mismatches 40; Indels 6; Gaps 4;

QY 146 EYVPLNIGAHFTTRSLTLCYEDTMLAAMF--SGRHYIPTDEGRYFIDRDGTHFGDVL 203
 DB 18 KYVELNVGQFYTTMGTLKHPGSKFSSEILSRARHY--KDAQGRFFIDRPGYFGLL 75
 QY 204 NPLRSGDLPERRRVAHYEAOYTAIGPLLEQENMOPKGEKYRQAETGLMPYKDH 262
 DB 76 DILRLGVQ-PTIYVPEVYQEAFTQIHLVKLIEDMPQIFGEQVARTQFLMGVFNRENT 134
 QY 263 ERIVEIARLAVORRKA 278
 DB 135 EYVLAARAAVAMS 150

RESULT 6

Q8TCA6 PRELIMINARY; PRT; 228 AA.

AC 08TCA6;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Hypothetical 26.5 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Strauberg R.;
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC022893; AAH22893.1;
 KW Hypothetical protein.
 SQ SEQUENCE 228 AA; 26540 MW; C8C5EA1D8F2B09B CRC64;

Query Match 11.9%; Score 211.5; DB 4; Length 228;
 Best Local Similarity 38.6%; Pred. No. 2.2e-08;
 Matches 51; Conservative 19; Mismatches 45; Indels 17; Gaps 2;

QY 148 VPLNIGAHFTTRSLTLCYEDTMLAAMFGSRHYIPTDEGRYFIDRDGTHFGDVLN 207
 DB 5 VTLNAGHLTYTSLTLTRYPDSMLGAMFGDPPARADPOGNFIDRDGPLEFYVNLFLR 64
 QY 208 SGDLP---PRERAVRYEAOYTAIGPLLEQENMOPKGEKYRQAFLGMPYKDHLE 264
 DB 65 TSELTPLDFKEFDLRKADFTQIEPLQCLNDPRPL-----YMDFFEE 110
 QY 265 IVEIARLAVOR 276
 DB 111 VVELSTRKLSK 122

RESULT 7

Q922M3 PRELIMINARY; PRT; 315 AA.

AC 0922M3;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Similar to tumor necrosis factor, alpha-induced protein 1 (endothelial).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC006935; AAH06935.1;
 DR InterPro: IPR000210; Pfam_P02.
 DR InterPro: IPR003131; K.tetra.
 DR Pfam: PF00224; K.tetra; 1.
 DR PROSITE: PS50097; BTB; 1.
 SQ SEQUENCE 315 AA; 35701 MW; 590AEF2D4E22D2D9 CRC64;

Query Match 11.7%; Score 208; DB 11; Length 315;
 Best Local Similarity 32.9%; Pred. No. 6.2e-08;
 Matches 54; Conservative 16; Mismatches 48; Indels 46; Gaps 4;

QY 77 SGQPAAGVMPGAPRARGVVTGRRPDSRRDQAMSSSDADDFLEPATPTATQA 136
 DB 5 SGDSVSSAVPAAATRTSF---KGASPSK----- 32
 QY 137 LPLPQEPPEVPLNIGAHFTTRSLTLCYEDTMLAAMFGSRHYIPTDEGRYFIDRDG 196
 DB 33 -----YKLVNAGHLTYTTLTQTL-TKQDTMLKAMSGMEVLTDEGWLIDRCG 81
 QY 197 THFGDVLNFRSGDLP---PRERAVRYEAOYTAIGPLLEQ 237
 DB 82 KHFGIIVNIRDGVPLPESRREIELLADEKYYLVQGLLEFG 125

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RESULT 8
ID 096S00 PRELIMINARY; PRT; 310 AA.
AC 096S00;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2002 (TEMBLrel. 19, Last sequence update)
DE 01-MAR-2001 (TEMBLrel. 20, Last annotation update)
DE CCNA FLJ14637 fls, clone NT2R2001327, moderately similar to tumor
DE necrosis factor, alpha-induced protein 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A.
RA Isegel T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027543; BAB55188.1;
DR InterPro: IPR000210; BTF_POZ.
DR InterPro: IPR003131; K_tetra.
DR Pfam: PF02214; K_tetra; 1.
DR PROSITE: PSS0097; BTF; 1.
SQ SEQUENCE 310 AA; 35042 MW; BA79F680F6920CF CRC64;

Query Match 11.6%; Score 206; DB 4; Length 310;
Best Local Similarity 32.3%; Pred. No. 8.6e-08;
Matches 53; Conservative 18; Mismatches 47; Indels 46; Gaps 4;

QY 77 SGPAAAGVMPGARRAGVYVGTGREPDSRRQDGMSSSDAEDDFLEPATPTAQGHA 136
DB 2 SGEVSSAVPAAPAAATRTTSF---KGTSPSK----- 29
QY 137 LPLLPQEPPEVVPINIGAHFTTRISTKCYEDTMAMFSGRHYIPDSEGRYFIDRG 196
DB 30 -----YVKLVNGALYYTQMQL-TKODTMKMFSGRMEVLTDSGWLIDRCG 78
QY 197 THEGDVLFNLSGDLF---PRERVAAYKEAQYVAGPILGLE 237
DB 79 KHEFTILNLYLDGAVLPESRREIELAEAKYYLVQGLVEECQ 122

RESULT 9
ID 09H3F6 PRELIMINARY; PRT; 313 AA.
AC 09H3F6;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2002 (TEMBLrel. 16, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE MSTP028.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A.
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hul R.T.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113308; AAG39279.1;
DR InterPro: IPR000210; BTF_POZ.
DR InterPro: IPR003131; K_tetra.
DR Pfam: PF02214; K_tetra; 1.
DR SMART: SM00225; BTF; 1.
DR PROSITE: PSS0097; BTF; 1.
SQ SEQUENCE 313 AA; 35432 MW; 199AF07A30D5BCA6 CRC64;

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Query Match 11.6%; Score 206; DB 4; Length 313;
Best Local Similarity 32.3%; Pred. No. 8.7e-08;
Matches 53; Conservative 18; Mismatches 47; Indels 46; Gaps 4;

QY 77 SGPAAAGVMPGARRAGVYVGTGREPDSRRQDGMSSSDAEDDFLEPATPTAQGHA 136
DB 5 SGEVSSAVPAAPAAATRTTSF---KGTSPSK----- 32
QY 137 LPLLPQEPPEVVPINIGAHFTTRISTKCYEDTMAMFSGRHYIPDSEGRYFIDRG 196
DB 33 -----YVKLVNGALYYTQMQL-TKODTMKMFSGRMEVLTDSGWLIDRCG 81
QY 197 THEGDVLFNLSGDLF---PRERVAAYKEAQYVAGPILGLE 237
DB 82 KHEFTILNLYLDGAVLPESRREIELAEAKYYLVQGLVEECQ 125

RESULT 10
ID 096SAL PRELIMINARY; PRT; 329 AA.
AC 096SAL;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2002 (TEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE TNFAIP1-like protein.
GN FKSG86.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A.
RA Wang Y.-G., Gong L.;
RT "Cloning and characterization of FKSG86, a novel gene encoding a
RT TNFAIP1-like protein."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY027918; AAK27301.1;
DR InterPro: IPR000210; BTF_POZ.
DR InterPro: IPR003131; K_tetra.
DR Pfam: PF02214; K_tetra; 1.
DR PROSITE: PSS0097; BTF; 1.
SQ SEQUENCE 329 AA; 36371 MW; 61092C2B0E81EA2D CRC64;

Query Match 11.5%; Score 204; DB 4; Length 329;
Best Local Similarity 41.2%; Pred. No. 1.3e-07;
Matches 56; Conservative 19; Mismatches 41; Indels 20; Gaps 7;

QY 123 LEPAATPTAQGHAL---PLLPQEPPEVVPINIGA-HFTTRISTKCYEDTMAMFS 177
DB 16 LEAPKPSGLEPGPAAYGKPLTPNS--KYVKLVNGSLHYTT-LRTL-TGODTMKAMFS 71
QY 178 GRHTIPDSEGRYFIDRGTHFGDVLNLSGDLFPRERVAAYK---EAQYVAGPILGLE 234
DB 72 GRVEVLIDAGGWLIDSGRHFHTLNTLRDGSVLPPESTHELGLLEARYIVQGLIE 131
QY 235 -----OLENMQPL 242
DB 132 DCOLALQKRETSPL 147

RESULT 11
ID 08WZ19 PRELIMINARY; PRT; 329 AA.
AC 08WZ19;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Hypothetical 36.4 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289573; AAL55757.1;
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR003131; K_tetra.
DR Pfam: PF02214; K_tetra; 1.
DR SMART: SM00225; BTB; 1.
DR PROSITE: PS50097; BTB; 1.
DR Hypothetical protein.
SQ SEQUENCE 329 AA; 36357 MW; 17A8AC2DBE81E78 CRC64;

Query Match 11.5%; Score 204; DB 4; Length 329;
Best Local Similarity 41.2%; Pred. No. 1.3e-07;
Matches 56; Conservative 19; Mismatches 41; Indels 20; Gaps 7;

QY 123 LEPAATPAAGAGAL---PLAQEPPEVVPINIGGA-HFTTRISTLCYEDIMLAFMS 177
DB 16 LEAPKPSGLEGPAAYGLKPLTPMS--KYVYLVGSGSLHYTT-LRTL-TGDDTLMKAFMS 71
QY 178 GRHYFTDSEGRYFIDRDGTHFGDVLNFRSGDLPPREVRAYRK---EAQYTAIGPILTE 234
DB 72 GRVETLIDAGGWLIDRSGRHFGTILNLDGVSPLPESTRELEGLGEARYIVQGLIE 131
QY 235 -----OLENQAPL 242
DB 132 DQALAQKRETLSP 147

RESULT 12
Q18986 PRELIMINARY; PRT; 220 AA.
AC 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DR D2045.8 protein.
GN D2045.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd C.R.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RT none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology";
RL Science 282:2012-2018(1998).
DR EMBL: Z35639; CAAG4696.1;
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR003131; K_tetra.
DR Pfam: PF02214; K_tetra; 1.
DR SMART: SM00225; BTB; 1.
DR PROSITE: PS50097; BTB; 1.
DR PROSITE: PS50097; BTB; 1.
SQ SEQUENCE 220 AA; 25651 MW; D4E755FBBF7D3296 CRC64;

Query Match 11.2%; Score 200; DB 5; Length 220;
Best Local Similarity 35.6%; Pred. No. 1.6e-07;
Matches 64; Conservative 22; Mismatches 46; Indels 48; Gaps 10;

QY 123 LEPAATPAAGAGALPLLPQEPPEVVPINIGGAHFTTRISTLCYEDIMLAFMSGRHYI 182
DB 1 MERST-----IVKLDVGGKIFKTTIFIL-CKHDSKMTMCTDVPV 40

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QY 183 PNDSEGRYFIDRDGTHFGDVLNFRSGD---LPPRE-VRATYKNOYAIQPLIEQLENM 239
DB 41 TNKEBSVFIIDRDSKRRLLINFLNRDQIALPDSRDREYLAARSLPLLE----- 95
QY 240 OPLKGEKVRQAFGLMPYKDYKHLERIVELARVORAKAPAKLSLPPMSLMVLIKMP 299
DB 96 --LCGERLEBS---LNNYI--HLVSTV---LEA--KKIIPATEKPI-----VYKRLP 135

RESULT 13
QY99F4 PRELIMINARY; PRT; 301 AA.
AC 09Y9F4.
DT 01-MAY-2000 (TREMblrel. 13, Created)
DE 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DR CG10465 protein (NES7120p).
GN CG10465.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Finnkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borzova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu X., Guan P., Harris K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iobagwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,
RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M.C., Skupski M.P., Smith T.,
RA Splitter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RA Stapleton M., Brocksstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guatin H., Krcmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Paclob J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

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RA Celniker S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003787; AAF57336.1;
 DR EMBL: AF071521; AAL49143.1;
 DR Flybase: FBgn0033017; CG10465.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR003131; K_tetra.
 DR Pfam: PF02214; K_tetra.1.
 DR SMART: SM00225; BTB.1.
 DR SEQUENCE 301 AA; 34048 MW; 4BEC83E6B70258F4 CRC64;

Query Match 11.0%; Score 196; DB 5; Length 301;
 Best Local Similarity 31.3%; Pred. No. 4.7e-07;
 Matches 62; Conservative 32; Mismatches 76; Indels 28; Gaps 6;

QY 139 LLPQEPPEVPLNIGAHFTRLSTLRCEYDTMLAMFSGRIYPTDSEGRFIDRGTH 198
 DB 12 LKGGHSGYLKLVNGGHLYTTTIGTLTKNDYMLSMFSGRMVELYDSGWLIDRCGNH 71
 QY 199 FGDIYVNFARSGDLP---PRERAVYKKEQVYAIGPLLEOLE-----NMQP-----L 242
 DB 72 FGIILNYLRDGVPLPETNKEIAELAEKKYCTELAISCEALYAHOPKPCRIPLI 131
 QY 243 KGEKVAFLGLMPYKDHLEIVEIARLAVQKARPAKLSLTPSWLMSVLKMPGV 302
 DB 132 TSGKEQLLISVS-----LKPAVILVYQROKNNKSYSTSDNLK-NIELEDKL 180
 QY 303 TSWINAEERLYLEPPIGP 320
 DB 181 SLRFN-ERILFIKDIYIGP 197

RESULT 14

Q96P93 PRELIMINARY; PRT; 329 AA.
 AC Q96P93;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Polymerase delta-interacting protein 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21477421; PubMed-11593007;
 RA He H., Tan C.K., Downey K.M., So A.G.;
 RT "A tumor necrosis factor alpha- and interleukin 6-inducible protein
 RT that interacts with the small subunit of DNA polymerase delta and
 RT proliferating cell nuclear antigen."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:11979-11984(2001).
 DR EMBL: AF401315; AAL14962.1;
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR003131; K_tetra.
 DR Pfam: PF02214; K_tetra.1.
 DR PROSITE: PS50097; BTB.1.
 SQ SEQUENCE 329 AA; 36395 MW; D356490B48995187 CRC64;

Query Match 10.8%; Score 193; DB 4; Length 329;
 Best Local Similarity 37.5%; Pred. No. 8.9e-07;
 Matches 51; Conservative 22; Mismatches 43; Indels 20; Gaps 6;

QY 123 LEPATPTATQAGHAL---PLLPQEPPEVPLNIGAHFTRLSTLRCEYDTMLAMF 177
 DB 16 LEAPKPSGLGEPAAVGLKPLFPNS--KYKLVNCGSLHYTTLITLNG--QDTMLKAMFT 71
 QY 178 GRHYITDSEGRFIDRGTHFDVNFARSGDLPPEERAVYK---EAQYVAGPLLE 234
 DB 72 GRLEVLTDAGSWVLIDRSGRHFGTILNYLDGSSVPLPESTKEIGELLGEARTYLVQGLIE 131
 QY 235 -----OLENMQPL 242

DB 132 DCOLALQOKRETTISPL 147

RESULT 15

Q8W0N2 PRELIMINARY; PRT; 333 AA.
 ID Q8W0N2;
 AC Q8W0N2;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical 36.2 kDa protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-CERVIX;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC019929; AAH19929.1;
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR003131; K_tetra.
 DR Pfam: PF02214; K_tetra.1.
 DR SMART: SM00225; BTB.1.
 DR KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 333 AA; 36219 MW; 657EB1B8167D5F6B CRC64;

Query Match 10.8%; Score 192.5; DB 4; Length 333;
 Best Local Similarity 30.2%; Pred. No. 9.9e-07;
 Matches 74; Conservative 28; Mismatches 98; Indels 45; Gaps 9;

QY 123 LEPATPTATQAGHAL---PLLPQEPPEVPLNIGAHFTRLSTLR 164
 DB 36 LTASTOFTCHGSSAFSLVSPLYKISPPVSPSPSFGAPVLNVCGLYSTLETL 95
 QY 165 RCYEOTMLAMFSGRIYPTDSEGRFIDRGTHFDVNFARSGDLPPEERAVYK 218
 DB 96 TRFDSMIGAEFRAGTTPPNNLSGGGHYFIDRGKAFRLNLRGLDLPKRGYET 155
 QY 219 AVYK-EAQYVAGPLLEQLENNQPKGEKVAFLGLMPYKDHLEIVEIA----- 269
 DB 156 ALIRAEADFYQIRPLDLALRELAOGTPAPYA--ALLHADVDVSPRLVHFSARGRPHY 213
 QY 270 RLRAVQKARPAKLSLTPSWLMSVLKMPGVTSWINAEERLYLETPIGERONNEKS 329
 DB 214 ELSSVOVDTPANLECTDSEICGALRARF--GYASGDRAEGSPHFLIENAPR----- 263
 QY 330 PVOLP 334
 DB 264 FVELP 268

Search completed: February 12, 2003, 11:08:34
 Job time : 36 secs